The Phylogeography of Murid Rodents from Tarutao National Park, Satun Province, Southern Thailand

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ABSTRACT

Order Rodentia is by far the most specious of all mammals worldwide. Most of the species in this order are known to be disease carries, pests, seed dispersers as well as food for both humans and other wildlife. The majority of the species in order rodentia fall in the Family Muridae. The biogeography and taxonomic status of the members of the species in this family in Southeast Asia (especially those from islands of the region) is still poorly known. In this study, both an ecological and a historical biogeographic study of Murid rodents were conducted on five islands (Tarutao, Adang, Rawi, Yang and Butong Islands) in Tarutao National Park located off the west coast of Thailand.

Four species of murid rodents were found in the National Park, namely *Rattus tanezumi*, *Maxomys surifer*, *Leopoldamys sabanus* and *Niviventer cremoriventer*. *M. surifer* was found to be the most abundant (48%) and was found on Tarutao, Adang and Rawi Islands only. It was closely followed by *R. tanezumi* (41.3%) which was widespread on all the five Islands. *N. cremoriventer* (2.6%) was found on Tarutao and Rawi Islands while *L. sabanus* (7.7%) was only found on Tarutao Island.

The species-area relationship, species-isolation relationship and nestedness of these species in Tarutao Island were assessed. The results showed that the species of murid rodents on the five Islands had a perfectly nested pattern of distribution with the smaller and more isolated islands have a subset of the species found on the larger and less isolated Islands. The species richness on the Islands was highly correlated to the area ($r^2 = 0.882$; df = 1,3; $p = 0.018$) and not correlated to the relative isolation of the Islands from the mainland ($r^2 = 0.474$; df = 1,3; $p = 0.198$). However, the species richness was not significantly correlated to the isolation because except for Tarutao the other four Islands were located close to each other hence having almost equal relative isolation from the mainland.

In order to elucidate the phylogenetic relationships of the murid species on the Islands within the National Park and also with their mainland relatives, a phylogeographic study of these murid rodents’ species was undertaken. This study used a multi-disciplinary approach of morphological, morphometric and two mitochondrial (cytochrome *b* and cytochrome c oxidase) and one nuclear (Inter Retinoid Binding Protein (IRBP)) DNA sequences. *R. tanezumi* and *M. surifer* were used as model species for this study. The results showed that *R. tanezumi* had complex phylogenetic relationship within the Islands and also with the mainland relatives. On the other hand, the results for *M. surifer* were interesting in that the populations on different Islands and the mainland had different haplotypes and grouped in distinct separate clades based on the mitochondrial genes. The divergence times were also estimated for both species and showed a very deep vicariant event separating the population long before the Islands were isolated from the mainland approximately 8, 500 years ago.

This study presents a most extensive study of the murid rodents in Tarutao National Park and probably one of the first most exhaustive studies of murid rodents on Islands in Southeast Asia. From the results, it is recommended that more phylogeographic studies of murid rodents on Islands in Thailand and Southeast Asia should be further conducted at a larger scale. This would help to understand the taxonomic status of the Islands species in relation to their mainland relative and might increase the number of murid rodents in the region which are still thought to be underestimated. Such studies would also help to understand the historical biogeography of the region which is also still poorly understood.

CONTENTS

List of Tables

Standard error estimate(s) are shown above the diagonal and were. obtained by a bootstrap procedure (1000 replicates).

List of Figures

List of Figures (Continued)

List of Figures (Continued)

List of Figures (Continued)

List of Figures (Continued)

CHAPTER 1

INTRODUCTION

Phylogeography is a sub discipline of biogeography concerned with the study of principles and process governing the geographical distributions of genealogical lineages, especially those at the intraspecific level (Avise 1998). The main aim of phylogeographers is to try to reconstruct and understand the origin, dispersal and extinction of living organisms. Biogeography in itself is “defined as the as the science that attempts to document and understand spatial patterns of biological diversity. This entails studies of all patterns of geographic variation in nature – from genes to entire communities and ecosystems – elements of biological diversity that vary across geographic gradients including those of area, isolation, latitude, depth, and elevation” (Lomolino *et al*. 2006a). From this definition of biogeography it can be deduced that is a very broad field of study which integrates many factors into one discipline. Therefore, this broad field can be divided into two many categories namely; historical and ecological biogeography.

Phylogeography falls under historical biogeography and this started more than two decades ago (Avise *et al*. 1987) and ever since this field has been growing at a faster rate (Avise 1998, 2000, 2009) and in the recent years the use molecular data in this field has helped to refine morphology-based methods in biogeography due to five main reasons (Lohman *et al*. 2011); firstly because molecular data generally offers a large number of characters that can help to determine relationships among taxa; secondly, molecular data the confidence in the strength of relationships can be examined; thirdly delimitation of species boundaries among taxa which are morphologically very similar (cryptic species) can be ascertained; and fourthly due advancements in techniques the divergence times among taxa can be estimated using molecular clocks and finally but not the least relative probabilities of different evolutionary hypotheses can be gauged (Avise 2000, 2009, Knowles 2009).

The use of DNA material in both species delineation and identification is a powerful tool for a wide range of mammals in Southeast Asia, hence sequencing of tissues of mammals from this region should be of high importance in understanding speciation processes as many taxa are wide spread with high levels of biogeographic separations (Francis *et al*. 2010). However despite phylogeography being a powerful taxonomic tool and coupled with the fact that Southeast Asia harbors many hotspot of biological diversity (Myers, *et al*. 2000) Phylogeographic studies in this region have remained behind when compared with other regions of the world (Sodhi and Liow 2000) therefore, it can be assumed that the biological diversity in this region may be still underestimated and once such tools are applied to many taxa more species are likely to be discovered and also this will help to understand the past distributions of the habitats in the region given that the sea levels have been rising and reducing in the past (Voris 2000). Based on this information, it is important that "future phylogeographic work in Southeast Asia should be given a priority and this will require analysis of fast evolving markers and extensive sampling of forest-dependent taxa throughout the region to understand the current distribution of taxa and the past distribution of habitats across the Sunda Shelf during the Pliestocene period (Lohman *et al*. 2011).

The second part of biogeography – ecological biogeography – "attempts to account for the present distributions and geographic variation in diversity in terms of interactions between organisms and their physical and biotic environments" (Lomolino *et al*. 2006a). Under this category comes island biogeography with its famous theory of the equilibrium model of island biogeography initially proposed in the 1960s (MacArthur and Wilson 1967) to explain different factors that affect taxa in isolated natural habitats. It also worthy to note that this theory has been also extended to other island-like habitats such as mountains, lakes, fragmented forests (Schmidt and Jensen 2003, Schmidt and Jensen's 2005, Sahney *et al*. 2010).

This equilibrium theory of island biogeography basically includes three main characters which are the species-area relationship, species-isolation relationship and species turnover. The first two relationships are explained in details below because they will be tested in this study. It is also worthy to make mention that studies in Southeast Asia to test these characteristics of the equilibrium theory are very scarce despite the region being rich with hundreds of islands. This leaves a gap for study in the future to test these relationships in different taxa in the region. Only a few studies have been conducted so far in the region such as those by Heaney (1978) and Meijaard (2003). Other trends have also been observed of insular taxa including the island rule – the tendency of large mammals to become smaller on islands and small mammals becoming giants on islands – and the nestedness distribution of insular taxa – were taxa on small and more isolated islands tend to be subset of the more species rich islands. These are also looked at in details in chapter 2.

Therefore, in this study we tried to look at both the historical and ecological parts of biogeography of the murid rodents in Tarutao National Park. From an ecological biogeography point of view, we assessed the biogeography of the murid rodents in the National Park by assessing the species-area relationship, species-isolation relationship and nestedness distribution. Later we looked at historical biogeography aspect were we selected two species as models and conducted a comparative phylogeographic study based on a multi-disciplinary approach of morphological, metrics, mitochondrial and nuclear DNA sequences to elucidate the phylogeography of murid rodents from the islands found in Tarutao National Park and also compare them with their mainland relatives to try to understand their evolutionary history.

This study thus is the most extensive study of the murid rodents in Tarutao National Park and it we hope that it will help to increase the knowledge of the murid rodents present in the National Park and also because these organisms have been known to be carriers of diseases this can be used as a baseline study in any future epidemiological studies especially that many tourists visit most of the islands in this National Park it is very important to know the species of both murids and the parasites they carry so that in case of any breakout of some disease related to these parasites (zoonoses) it would help to combat such break outs. Also this is the first study which will try to reassess the taxonomic status of the murid rodents in this National Park since it became an ASEAN Heritage National Park. Finally we hope that the results can be used to help advice on the conservation of the murid rodents if they are different from their mainland relatives bearing in mind that insular rodents are more prone to extinction because of the limited area and resources.

OBJECTIVES AND RESEARCH QUESTIONS

OBJECTIVES:

1. To assess the species diversity and distribution pattern of murid rodents in Tarutao National Park.
2. To test some biogeographic theories of species-area relationship and species-isolation relationship, nestedness and the island rule on murid rodents in Tarutao National Park.
3. To assess the phylogenetic relationships within populations of murid rodents on the islands in Tarutao National Park and also with the mainland populations, using morphological, metric and molecular data.

RESEARCH QUESTIONS:

1. How many species of murid rodents are found in Tarutao National Park and does their distribution patterns conform to the species-area relationships, species-isolation relationship and nestedness distribution?
2. Does the area and relative isolation of an island influence the number and size of murid rodent species present on that island?

Hypothesis: the area of an island and its distance from other islands and the mainland influence the number and size of murid rodent species found on that island.

3. How are the murid rodents populations phylogenetically related to each other within the islands in Tarutao National Park and to the mainland populations?

Hypothesis: if the populations of murid rodents on the islands in Tarutao National Park have been separated from the mainland population and from other island populations for a long time and there is little/no gene flow between the populations, then there should be some morphological and/or genetic differences between the populations.

CHAPTER 2

LITERATURE REVIEW

1. GENERAL INFORMATION ABOUT MURID RODENTS

Taxonomy and Diversity of Murid Rodents in Thailand

Murid rodents are classified under;

Kingdom: Animalia
  Phylum: Chordata
    Class: Mammalia
      Order: Rodentia
        Superfamily: Moroidea
          Family: Muridae (Illiger, 1811)
            Subfamilies: (1) Deomyinae
              (2) Gerbillinae
              (3) Leimacomyinae
              (4) Murinae
              (5) Otomyinae

Class Mammalia is diverse in both form and function. It comprises members as tiny as Kitti's Hog-nosed Bat (*Craseonycteris thonglongyai*) and the white-toothed pygmy shrew (*Suncus etruscus*) to as large as the blue whale (*Balaenoptra musculus*) and the African bush/savanna elephants (*Loxodonta africana*). This wide range of size gives this class the ability to consist of many species. According to Wilson and Reeder (2005), class mammalia has approximately 1,229 living genera divided into 5,416 species. Order Rodentia is by far the most specious order all of extant mammals, with 481 genera and 2,277 species presently recognized, or approximately 42% of world wide mammalian biodiversity as shown in figure 1. There are only 3 families of living rodents, comprising of Sciuridea, Muridae, and Hystricidae (Musser and Carleton 2005).

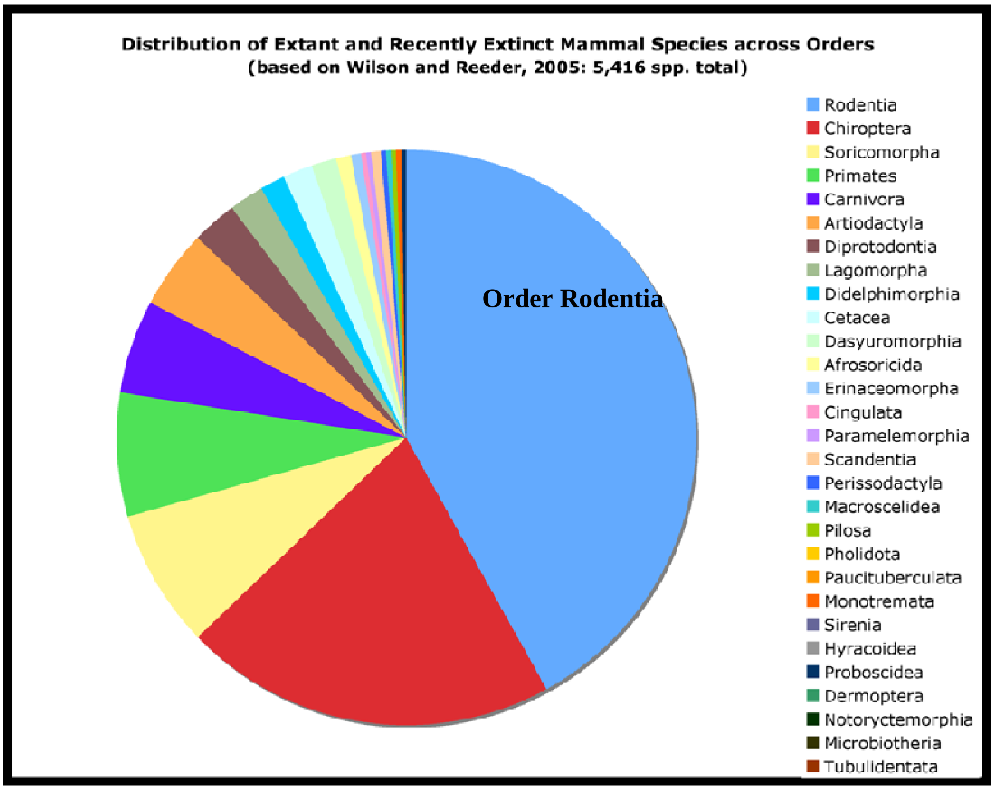

Figure 1: The global distribution of extant and recently extinct mammal species across orders.

The family Muridae is the largest of all rodents worldwide comprising 150 genera and 730 species. According to recent classifications, this family includes five subfamilies (Musser and Carleton 2005, Vaughan *et al*. 2011) namely: (1) Deomyinae (spiny mice), (2) Gerbillinae (gerbils and their relatives), (3) Leimacomyinae (groove-toothed forest mice), (4) Murinae (old world rats and mice), and (5) Otomyinae (vlei rats and whistling rats). This diversity developed relatively recently, within the last 15 to 20 million years, after an initial appearance in the middle Miocene (Vaughan *et al*. 2011).

Nabhitabhata and Chan-ard (2005) and the Office of Natural Resources and Environmental Policy and Planning (2007) show that Thailand has a total of 302 extant species of mammals currently recognized. About 27% of extant mammalian species in Thailand are in the order Rodentia which is second in diversity richness to the order Chiroptera (38%) (Chaimanee 1998). They are represented by all three families, the Sciuridae, Muridae, and Hystricidae (Musser and Carleton 2005). As of 1998, the relative abundance of extant rodent species in Thailand could be represented as; “26 species (39%) of Sciuridae, including 16 species (24%) of Sciurinae (squirrels) and 10 species (15%) of Petauristinae (flying squirrels); 39 species (58%) of Muridae, which included 35 species (53%) of Murinae, 1 species (1%) of Arvicolinae, 3 species (4%) of Rhizomyinae and 2 species (3%) of Hystricidae” (Chaimanee 1998). Among these extant rodents are two endemic rodents in Thailand, which both belong to the subfamily Murinae (i.e. *Niviventer hipoon* and *Leopoldamys neilli*) (Marshal 1976) in (Chaimanee 1998). Despite this knowledge, the composition of the local communities of living rodents is still poorly known in Thailand (Chaimanee 1998).

Tate (1947) and Francis (2008) suggests that in Southeast Asia, all the species of the family Muridae are in the subfamily Murinae. According to Chaimanee (1998), “About 35 species of murine rodents are found in Thailand, 16 species (46%) are restricted to the north of the Isthmus of Kra (Indochinese sub region): *Vandeleuria oleracea, Chiromyscus chiropus, Leopodolmys edwardsi, L. neilli, Berlymys berdmorei, N. confucianus, N. langbianis, N. hinpoon, Rattus losea, R. nitidus, R. sikkimensis, Mus shortrigei, M. pahari, M. cookie, M. cervicolor* and *M. caroli.* Five species (14%) are restricted to peninsular Thailand south of the Isthmus of Kra (Sundaic sub region): *N. cremoriventer, Maxomys rajah, M. whiteheadi, Sundamys muelleri and R. tiomanicus.* Fourteen species (40%) are distributed in both sub regions.” This distribution of the murid rodents in Thailand can be expressed figuratively as shown in figure 2. However, there is no clear literature stating how many species of murid rodents are found on the islands of Thailand.

Figure 2: Map of the distribution of murid rodents in Thailand.

Recently Chaval (2011) compiled documents for field identification of South East Asian Murines and increased the number of species in the subfamily Murinae in Thailand to 37 listing 2 species in genus *Bandicota* (*Bandicota indic*a and *B. savilei*), 2 species in genus *Berylmys* (*Berylmys berdmorei* and *B. bowersi*), 2 species in genus *Hapalomys* (*Hapalomys delacouri* and *H. longicaudatus*), 3 species in genus *Leopoldamys* (*Leopoldamys edwardsi*, *L. sabanus* and *L. neilli*), 3 species in genus *Maxomys* (*Maxomys surifer*, *M. rajah* and *M. whiteheadi*), 7 species in the genus *Mus* (*Mus caroli*, *M. cookii*, *M. cervicolor*, *M. fragilicauda*, *M. musculus* *castaneus, M. pahari* and *M. shortridgei*), 6 species in genus *Niviventer* (*Niviventer cremoriventer, N. langbianis, N. hinpoon, N. fulvescens, N. confucianus* and *N. tenaster*), 2 species in the genus *Chiromyscus* (*Chiromyscus chiropus* and *C. gliroides*), 1 species in genus *Sundamys* (*Sundamys muelleri*), 1 species in genus *Vandeleuria* (*Vandeleuria oleracea*), and 8 species in the genus *Rattus* (*Rattus norvegicus, R. nitidus, R. exulans, R. tanezumi, R. losea, R. andamanensis, R. tiomanicus* and *R. argentiventer*). I have decided to give the species list above after Chaval (2011) because he uses the recent taxonomic names and also some species that where misidentified previously have been corrected based on molecular data, for example, what used to be called *R. rattus* in Thailand has now been found to be *R. tanezumi*. Therefore, Chaval (2011) gives a more updated list and taxonomy of Murine species in Southeast Asia and Thailand in particular.

Common characteristics of murid rodents

In general, all Murid rodents can be recognized by their dental formula of i. 1/1, c. 0/0, p. 0/0, m. 3/3 =16, the incisors are large, curved and chiseling in both the upper and lower jaws and because the canines are absent, it means they have a wide toothless gap which varies with species (diastema) before the cheek teeth (molars) (Ellerman 1941, Francis 2008). These features can be seen in figure 3.

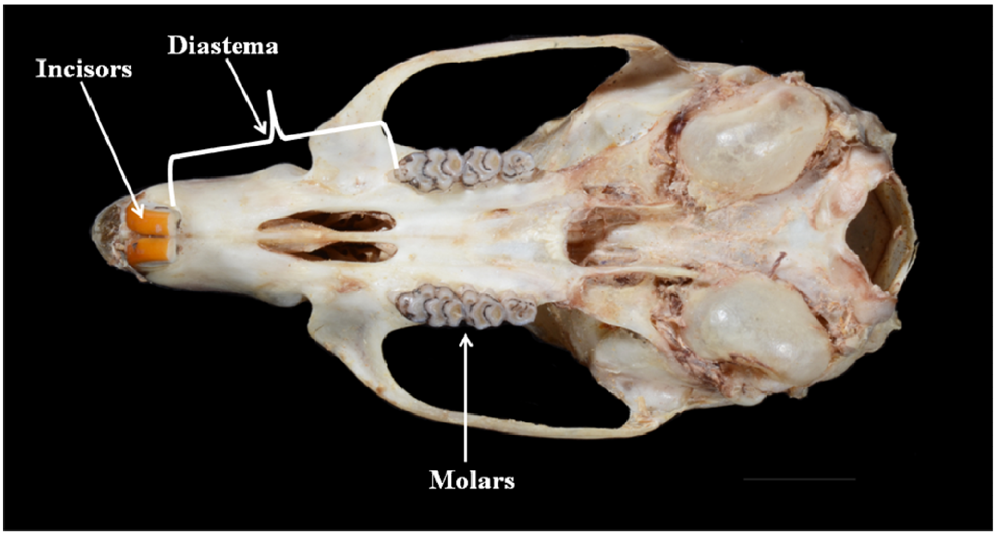

Figure 3: Common characters of all murid rodents.

The roles of murid rodents in the ecosystem

Murid rodents play many important roles in the ecosystem. They are important agricultural pests, seed dispersers, disease vectors and sources of food for wildlife and humans (Lunde and Son 2001).

Murids in Thailand have been known to be carriers of some diseases that have been transmitted to humans in the past. For example according to McNeely and Lekagul (1988), "rats of Thailand are the reservoir of a human disease, scrub typhus. The causative *Rickettsia* lives in the blood of field rats and is carried by larval mites called chiggers, which bite rats and man alike. They are pale, delicate, tiny, spider-like animals that have only six legs. They are colored translucent yellow, cream, or red. Chiggers climb in the fur of rats, on grass stems in savannah areas of Thailand, and they lodge in patches inside the ears of rats. Plague, which is a bacterial disease of rats carried to man by the rat flea, *Xenopsylla cheopis,* is not found in Thailand, owing apparently to an insufficiency of fleas and lack of a sylvatic reservoir. We do have a potential plague flea, *Xenopysylla vexabilis*, which infests the wild *Rattus berdmorei.* On either side of the kingdom plague occurs in fleas affecting commensal *Bandicota indica, Rattus norvigicus, R. exulans*, *R. rattus,* and, oddly enough, *Crocidura murina.* During a high point in rabies prevalence several years ago, the journal *Nature* reported that great bandicoots of central and southeastern Thailand were found to harbor the virus. Attempts to repeat this observation have failed." From this citation, we can see that rats can cause harm to people. Therefore, I feel if we are to combat such diseases in case of an outbreak in future, we should understand the diversity of these rats in our locality hence the need to study the diversity of Murids, including on the islands of Tarutao National Park.

Furthermore, studies of rodents as disease carriers in Thailand have been carried out for a long time (Brown *et al.* 1978, Tingpalapong *et al*. 1978). In recent years there has been an increase in the number of publications on rodents as disease carriers especially murid rodents (Kitaoka and Suzuki 1983) and more recently by Kitaoka and Suzuki (1983), Pipitgool *et al*. (1997), Naigowit *et al.*

(2000), Nitatpattana *et al*. (2000), Wangroongsarb *et al*. (2002), Castle *et al*. (2004), Doungchawee *et al*. (2005), Herbreteau *et al.* (2005), Hugot *et al*. (2006), Sarataphan *et al*. (2007), Jittapalapong *et al*. (2008), Jittapalapong *et al*. (2009), Chaisiri *et al*. (2010, 2010b, 2012), Changbunjong *et al*. (2010), Ponlet *et al*. (2011), Rodkvamtook *et al*. (2011), and Herbreteau, *et al*. (2012). However, all these studies have focused on the mainland murid rodents and not on the islands populations. Therefore, this study will form a baseline for any future epidemiological or ecological study of murid rodents of Tarutao National Park.

Further evidence that identification of murids of Tarutao National Park will help to combat rodent-borne diseases if any erupts in future can be supported with a recent outbreak of leptospirosis that took place in a rural area in north-eastern Thailand and claimed 107 people between October-December 1997 while a total of 2,236 had to be treated for leptospirosis in this same year (Chokvivat 1998). However, in this scenario, we can conclude that the lack of information on rodent species lead to many people dying. As reported by Boonsong, *et al*. (1998) that “this incident was broadly covered in media and it drew fresh attention to the rodent problem. Although it is not clear which rodents species actually transmitted the disease, this incident emphasizes the need for a better knowledge of the epidemiology of rodent-borne disease in the region.”

One other major role that rodents play in an ecosystem but has remained largely overlooked and little research done is on their importance in the succession of forests (especially tropical rainforests). According to Steven and Marcel (1999), “through seed dispersal and predation, terrestrial mammals should be an important component of the mechanism that determines patterns of tree recruitment in tropical forests”. Although many people view rodents as being mainly seed predators, they at the same time disperse seeds due to the removal of the seeds from parent plants before eating, long consumption times and the ability of partially consumed seeds to germinate, makes them to also function as secondary dispersal agents (Wells and Bacgchi 2005) and also in dispersal of invasive plant seeds (Shiels 2010).

Results from a study in *Araucaria* forest, southern Brazil, showed that "rodents may be involved in the dispersal of three plant species, by defecation of viable seeds of two *Leandra* (Melastomataceae) species and also by removing the pulp of *Myrceugenia miersiana* (Myrtaceae) fruits without swallowing or damaging their relatively large seeds, thus, potentially increasing germination rates of *M. miersiana*" (Vieira *et al*. 2006). Reviews such as the one conducted by Corlet (1998), points out that mostly the literature often does not make a clear distinction between consumption of the pulp and the seeds. He further says that while most species of rodents seem to destroy most seeds, often discarding the flesh, the most detailed studies also report that, in some fruits, the pulp only is eaten and the seed dropped (Corlet, 1998 and the literatures cited there in). Such results can also be supported by another report in which a rodent, *Cerradomys subflavus*, was thought to be acting as a seed disperser of a palm, *Allagoptera arenaria*, a nurse plant species in southeastern Brazil (Grenha *et al*. 2010).

It is also worth noting that not only do rodents disperse seeds but there also some studies which give evidence for rodents as pollinators. For example "live trapped rodents (e.g. *Aethomys*) in southern Africa were found to carry large amounts of *Colchicum* (Colchicaceae) pollen on the fur of their snouts, and in their feaces" (Kleizen *et al*. 2008) and the same results were reported in the pollination of the African lily *Massonia depressa* (Hyacinthaceae) by rodents (Johnson *et al*. 2001). This phenomenon would be expected in many plants that have robust flowers that are dull in color, cup-shaped, have copious amounts of nectar, exerted styles and stamens and these are situated at ground level an adaptation for pollination by non-flying mammals (including rodents, marsupials and primates) (Rourke and Wiens 1977, Wiens and Rourke 1978, Wiens *et al*. 1983, Carthew and Goldingay 1997). Furthermore, in a study of microhabitat used by a tropical forest rodents, *Proechimys semispinosus*, in central Panama, it was found that this rodent was associated with younger forests (small trees and liana and lower canopies) and tree fall gaps within older forest and the conclusion was that it may have implications for the regeneration of local forest patches through their activities as seed predators and dispersers of seeds and arbuscular mychoorhizal fungi spores (Lambert and Alder 2000).

Therefore, based on the review of literature available, a flow chart can be used to summarize the importance of rodents on islands as below:

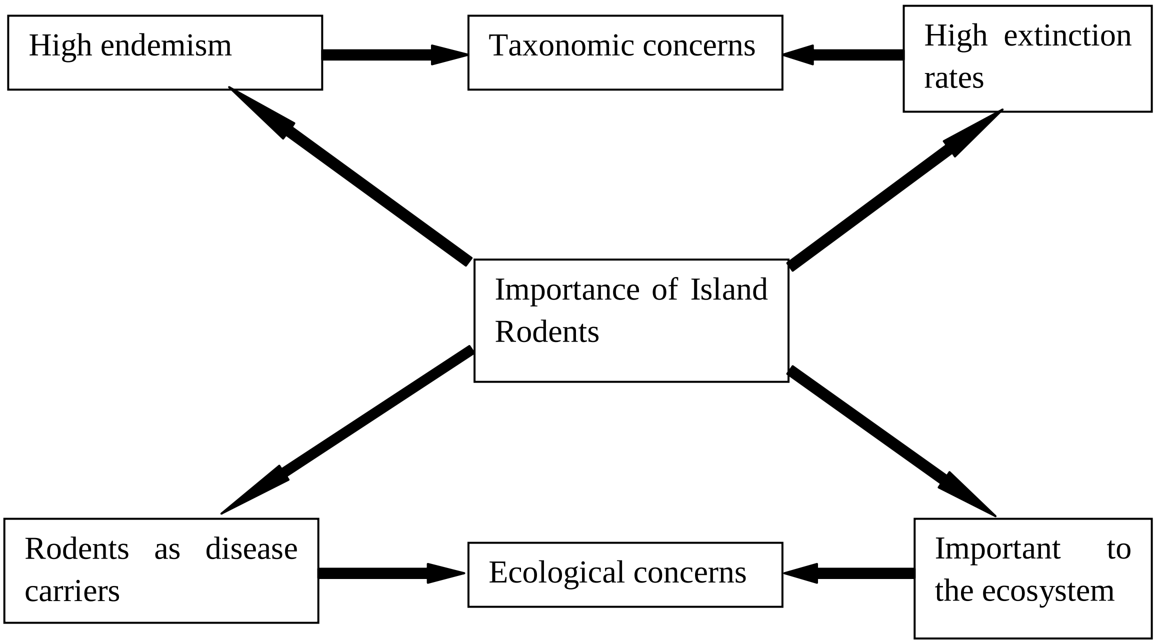

Figure 4: Flow chart summarizing the importance of island rodents in a broader view.

Habitat and feeding habits of murid rodents

Murid rodents (members of the family Muridae) occupy just about every type of habitat imaginable. They are known to live in dry sand deserts, wet tropical forests, agricultural fields, and the world's largest cities. Murids also inhabit alpine tundra at elevations exceeding 4,000 m and can be found in mine shafts more than 500 m below the earth's surface. Other habitats include shrub lands, grasslands, swamps, bogs, meadows, and every imaginable forest type (Nowak 1999). Murid rodents feed on almost everything. Mice mainly feed on fruits, grass seeds, and arthropods while rats mainly feeding on various fruits, dicot leaves and arthropods (Cole *et al*. 2000). Some rodents also feed on stems, roots of grass and herbs (Wang *et al*. 2003). Therefore, it can be concluded that rodents have a vast range of foods that they can consume. They are herbivorous, granivorous and omnivorous and perhaps this is the reason why they have been able to inhabit almost the whole globe.

Fecundity of murid rodents

Most rodents, including murids, have short gestation periods in which they produce large litters” (Nowak 1999). According to Pass and Freeth (1993) and University Animal Care Committee (2009) the basic biological data of the rat is that; the oestrous cycles lasts about 4-6 days, gestation lasts between 21-22 days and the litter size is about 6-14 pups, weaning age being about 20-21 days and the rat becomes sexually mature after about 7 weeks from birth and reproductive life lasts approximately for 8 months and they have a potential life span of about 2.0-3.5 years in captivity but probably the life span is less in nature where they are faced with challenges of limited resources and many predators (figure 5).

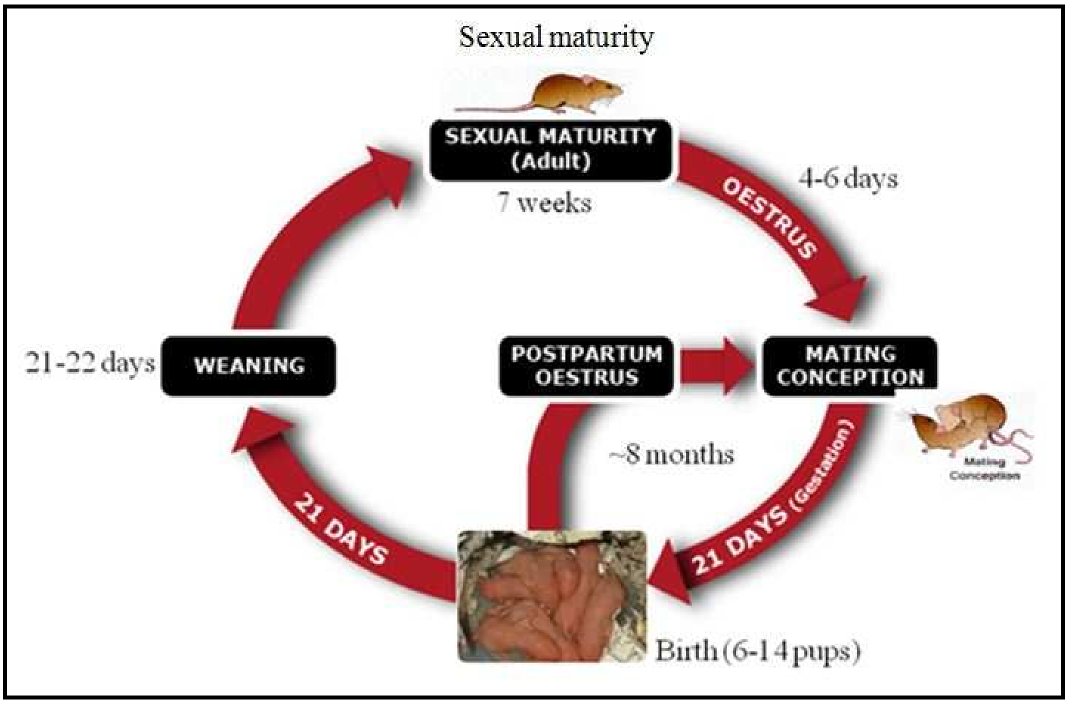

Figure 5: Basic life cycle of murid rodents. Modified from Pass and Freeth (1993).

Home range of murid rodents

According to Burt (1943) a home range is defined as “the area traversed by individuals of a species in their normal activities of feeding, mating, and caring for their young” while Blundell *et al.* (2001) defines a home range as “ the probability of locating an animal at a particular place by using a utilization distribution based on relative frequency of location”. However, “within a species, home-range size can vary due to factors such as sex, mass, age, and breeding condition of the individuals as well as habitat type, food availability, populations density, and season” (Wood *et al*. 2010). For example the home range values obtained by boundary strip method in of *Apodemus flavicollis* varied from 100 -2300m^2 while that of *A. agrarius* varied from 100-2400m^2 on mount Avala in Serbia (Vukićević-Radić *et al*. 2006), and Wood *et al*. (2010) estimated the home ranges of deer mouse in sage-steppe habitat and found that it varied from 360-5868m^2.

Further, Eiris and Barreto (2009) pointed out that home ranges of male and female marsh rats, *Holochilus sciureus*, ranged between 0.6 and 1.3 ha depending on the method of estimation. They thus interpreted their results that male-female range overlaps and possible agonistic interactions between males, suggest male territoriality and a polygenic mating system. However, males showed greater motility than females. “The total home size of female striped mice (*Rhabdomys pumilio*) varied from 0.06ha-0.8ha during the breeding season and varied from 0.06-0.8ha in the dry non-breeding season” (Schmohl 2008). However, the home ranges of island populations of rodents are smaller than in open systems (mainland) (Gliwicz 1980). More studies of the home ranges of rodents can be found in Clapperton (2006) and the references sited therein. Therefore, if considered in terms of length, the home range of rodents in general is less than 1km (García-Estrada *et al*. 2002).

Importance of insular rodents and their conservation and/or taxonomic implications

Today, the high endemism rates of insular animals and plants and their vulnerability to the introduction of alien species make insular biotas among the top conservation priorities. Despite islands attracting special attention of biologists since the time of Darwin and Wallace, the rodents of many large and small islands still remain to be studied. The high number of rodent species (more than 2050) and the high rate of endemism of rodent orders among mammals, coupled with lack of information on population status and often still questionable taxonomy, emphasize the priority for research on these animals. Scant attention has been paid to the conservation of rodents in general. This is particularly worrying when we consider island species which are particularly threatened (Amori and Clout 2003).

"Rodents species restricted to islands include at least 388 extant species worldwide (17.5% of all extant rodent species), classified in 127 genera and 10 families. Species of Muridae (258 species) and Sciuridea (54 species) are most widespread on islands. There are 83 currently recognized rodent genera entirely endemic to islands (corresponding to 197 species in total), representing 17% of all rodent genera. Only one family, Capromyidae (the hutias), is found only on islands, being endemic to the Caribbean region" (Amori *et al*. 2008). The islands with the highest number of endemic rodent genera are the Philippines (20), New Guinea (19), Sulawesi (12) and Madagascar (9) (Amori and Clout 2003).

It is clear that islands have been found to be associated with high proportion of endemic rodents. Actually Amori *et al.* (2008), stress that almost one in five of the world's nearly 2300 rodent species is an island endemic but because of little attention that has been directed to these animals by conservationists, insular rodents suffer from high rates of extinction and threats (caused mainly by habitat destruction, overhunting and introduced species). They further elaborate that rates of Quaternary extinction and current threat are especially high in the West Indies and the species-rich archipelagos of Southeast Asia, thus, efforts specifically targeted towards less conspicuous animals (e.g. insular rodents) may be necessary to stem large numbers of extinction in the future (Amori *et al.* 2008).

Hence, this study is important as it will help to recommend on the conservation efforts that should be directed to murid rodents in this National Park and which islands should be prioritized for their conservation. This is because murid rodents in Tarutao National Park have not been studied for a long time (including since it was declared an ASEAN Heritage National Park in 1984) as evident from the lack of sufficient and conclusive information on the rodents from this Marine National Park which is entirely comprised of islands in Thailand. It can therefore, be concluded that the study of murids from this Marine National Park have been neglected, this should be a sense of concern for taxonomists and conservationists.

It is important to assess the diversity of these murids because it is only when the species found in an area are known that we can start to think of conserving such species. Without the knowledge of the species, it is not possible to properly preserve them. Also when the species are known it is easy to prioritize which species should be serious protected to prevent their extinction (Mace 2004, Bates 2010). Further, "the role of sound systematics for setting priorities for biodiversity conservation is receiving increasing recognition. The present work provides some examples about how systematic ambiguities and uncertainties might affect conservation prospects for the most species-rich mammal order. A clear understanding of systematics is fundamental to protect the diversity of rodents, even though utilizing a higher-taxon approach" (Amori and Gippoliti 2003). Therefore, the importance of systematics in conservation cannot be overlooked.

In short the importance of this research can be summarized by saying that "taxonomists, with their identification guides, keys, databases, and specialist knowledge of particular animal or botanical groups, are uniquely qualified to identify, describe and thereby support the work of ecologists and conservationists. They can advise on priorities for species and site-based conservation and help monitor biodiversity loss from the impacts of climate change and habitat fragmentation. They can assess the spread of invasive alien species and identify the host species in the study of zoonoses" (Bates 2010).

Brief introduction to phylogeography

The term phylogeography was coined more than 20 years ago (Avise *et al*. 1987) and it is a sub discipline in biogeography that emphasizes historical aspects of the contemporary spatial distributions of gene lineages (Avise and Hamrick 1996). Therefore, in general terms, phylogeography can be defined as "a field of study concerned with principles and process governing the geographical distributions of genealogical lineages, especially those at the intraspecific level" (Avise 1998). The first decade of phylogeographic studies was based mostly (> 80%) on mitochondrial (mt) DNA because of its rapid evolution in populations of higher mammals and transmission through female organisms without intermolecular recombination and little of nuclear genes where used (Avise 1998).

The weakness of relying mainly on mtDNA alone was that empirical or theoretical treatments that addressed phylogenetic aspect of the spatial distributions of any genetic trait were overlooked because the matrilineal phylogeny (or any other allelic transmission pathway) represents only a small fraction of the total historical record with a sexual organismal pedigree. Thus, most recent phylogeographic studies use both mtDNA and nuclear genes to give a full understanding of an organism's history and distribution (Avise 1998, 2009, Brito and Edwards 2009). This combination of both mitochondrial and nuclear markers has increased the strength of molecular data to test phylogenetic and phylogenetic hypotheses and this has in turn highlighted the limitations of studies using only mtDNA as explained above and has also helped to identify many conflicting geographical patterns between these two sets of molecular markers in the past decade (i.e. mito-nuclear discordance) (Toews and Brelsford 2012).

Despite the debate on the reliance on mtDNA alone, most studies still use them (especially cytochrome *b*) because these gene is "important for understanding the evolutionary relationships among individuals, populations, and species" (Irwin *et al*. 1991) and also because the cyt-*b* gene has been used successfully to resolve relationships among and within species in a wide range of taxa for a long time (Reeb and Avise 1990, Bowen *et al*. 1994, Taberlet *et al*. 1998, Walker and Avise 1998, Rocha-Olivares *et al*. 1999, Weisrock and Janzen 2000, Castresana 2001, Farias *et al*. 2001, Johansson *et al*. 2002, Martin 2006, Rosli *et al*. 2011), in identification of species (Tsai *et al*. 2007) and its rates of evolution have been studies in some taxa (Irwin *et al*. 1991, Martin and Palumbi 1993, Castresana 2001).

Mitochondrial cyt *b* gene is mostly used in phylogeography (the study concerned with patterns and processes governing geographic distributions of genealogical lineages among and within closely related species) because it represents a mitochondrial DNA bridge between population genetics and systematics and also represents an interplay between vicariance and dispersal processes" (Avise *et al*. 1987, Bowen *et al*. 1994, Avise 1998, 2009). Further, according to Russo (2009), this "gene has successfully been used to investigate systematics relationships in a number of murid rodents" giving examples of Ducroz *et al.* (1998); Ducroz *et al.* (2001); Galewski *et al*. (2006); Patton and Smith (1992); Russo *et al.* (2006); Smith and Patton (1993, 1998); Verheyen *et al.* (1995, 1996). Therefore, it is based on this evidence that mitochondrial cytochrome *b* (cyt-*b*) was used in this study.

However, most researchers currently use a combination of mitochondrial and nuclear genes to reconstruct the lineage history of the individual. In this study, the nuclear Interphotoreceptor Retinoid Binding Protein (IRBP) gene was added to the mitochondrial genes (cyt-*b* and CO1 genes). A combination of mitochondrial cyt-*b* and nuclear IRBP genes to infer phylogenetic relationships has successfully been used in murine rodents from previous studies (Serizawa *et al*. 2000, Suzuki *et al*. 2000, Suzuki *et al*. 2003, Suzuki *et al*. 2004b, Lecompte *et al*. 2005, Veyrunes *et al*. 2005, Jansa *et al*. 2006) and more recently a combination of these genes has been used in Southeast Asian murine rodents (Pagés *et al*. 2010). These genes have also been used in other classes mammals such as in carnivores by Sato, *et al*. (2003)

Since its inception in 1987, phylogeographic studies have increased exponentially (Avise 2000, 2009). During this expansion of phylogenetic studies rodents have been studied in various regions of the world (Avise *et al*. 1983, Harris *et al*. 2000, Sullivan *et al*. 2000, Kuch *et al*. 2002, Brunhoff *et al*. 2003, Rambau *et al*. 2003, Albright 2004, Oshida *et al*. 2005, Palma *et al*. 2005, Nicolas *et al*. 2008a, Edwards 2009, Miranda *et al*. 2009, Bryja *et al*. 2010, Indorf 2010, Tollenaere *et al*. 2010, Alarcón *et al*. 2011, Bryja *et al*. 2012, Mouton *et al*. 2012, Nicolas *et al*. 2012, Konećny *et al*. 2013), in Asia (Suzuki *et al*. 2000, Suzuki *et al*. 2001, Suzuki *et al*. 2003, Suzuki *et al*. 2004a) and some studies have been in southeast Asia (Gorog *et al*. 2004, Shimada *et al*. 2007, Latinne *et al.* 2011).

However despite southeast Asia being a biodiversity hotspot (Myers *et al*. 2000), little attention has been given to it by phylogeographers since the inception of the term in 1987 to 2006 (Beheregaray 2008). Therefore, because of the high scientific interest in the region, more phylogeographic studies are needed and this might also increase the number of mammal species known in the region and also help resolve some taxonomic problems of species identification based on morphology like (Francis *et al*. 2010) like the case of *R. rattus* which for many years was identified based on morphology but with the advancement of molecular tools, it has now been found to represent a distinct Asian form, *R. tanezumi*, and not *R. rattus* (Pagés *et al*. 2010).

2. REVIEW OF SOME ISLAND BIOGEOGRAPHY THEORIES

Islands can be viewed as patches of the mainland separated by a form of barrier – e.g., water – and thus conducting a research islands is like conducting an artificial experiment, however, the only difference from an artificial experiment is that a research on an island is like an experiment without making any modifications to the study site. “Islands and other insular habitats, such as springs, lakes, and caves, are ideal subjects for natural experiments. They are well-defined, relatively simple, isolated, and numerous – often occurring in archipelagoes of tens or hundreds of islands. Just as conditions can be varied in artificial manipulative experiments, islands can vary in a number of environmental features (e.g., area, isolation, or presence of predators and competitors)" (Lomolino *et al*. 2006a) and for this reason ecologists have long been especially interested in islands (Pianka 1983).

Many studies have been conducted on mammals and other living organisms on islands and rules have evolved based on recurring general patterns of distribution of organisms. Such studies have given birth to theories that seek to explain these observations such as the species-area relationships, species-isolation relationships, species turnover (Lomolino *et al*. 2006a), island rule, nestedness etc. "The number of species found on an island, therefore, depends on a number of factors – not only its area and topography, its diversity of habitats, its accessibility from the source of its colonists, and the richness of that source, but also the equilibrium between the rate of colonization by new species and the rate of extinction of existing species. Many individual observations and analysis of such phenomena have been made over the past 150 years" (Cox and Moore 1993). Here I will explain some of the theories upon which the current research was based upon and try to assess these theories.

Firstly, I would like to discuss the species-area relationship. The species-area relationship is one of the most important and most frequently studied patterns in biogeography (Lomolino 1989) and was described by Schoener (1986) as "one of community ecology's few universal laws". According to Lomolino *et al.* (2006a), "it is one of the most general, best-documented patterns in nature" (citing Forster 1778; de Candolle 1985; Watson 1855; Jaccard 1902, 1908; Arrhenius 1921; Gleason 1922, 1926).

The species-area relationship is a theory that shows that "larger islands generally support more species of plants and animals than smaller ones. In fact, when plotted on a double log scale, the number of species in a given taxon typically increases more or less linearly with island size. In most cases, a tenfold increase in area corresponds to an approximate doubling of the number of species" (Pianka 1983). Based on this relationship, the Arrhenius equation or power model is used to express the species-area relationship and this is given as:

$$S = cA^z$$

Where S is the number of species or species richness, c is a fitted constant which varies between taxa and also between places, A is the area of the island(s) in question, and z is also a fitted constant that represents the slope when both S and A are plotted on logarithmic scales. Usually a log is taken on both sides of the above equation and the equation becomes as below with z as the slope (and this usually gives a linear relationship between area and species richness when plotted on a graph):

$$\log S = \log C + z \, .\log A$$

According to Pianka (1983), the value of z generally ranges from 0.24 to 0.33 on many different island systems with a larger value of z resulting from topographic diversity and spatial replacement of species or what he referred to as "island within island"; while lower values arise due to reduced replacement of species in space, as on very homogenous islands, continents, or subsamples of large islands.

Another pattern that is studied with respect to the fauna or flora of islands is the species-isolation relationship. This theory looks at why islands far from the mainland will support fewer plant or animal species as compared to those that are nearer to the mainland. Isolation of the island should therefore have a greater adverse influence on the diversity of non-volant mammals as compared to volant mammals because the former cannot fly as compared to the latter which can fly from one island to the other or from the mainland to the island sometimes aided by the wind. "Single, isolated islands far out in the ocean support fewer species than islands that are part of major archipelagoes or islands that are located nearer to continents. Assuming that the decline in species richness results from a decline in dispersal rates with isolation, the form of the species-isolation relationship should be a consequence of dispersal curves for the pool of species (potential colonists from the mainland)" (Lomolino *et al*. 2006a).

According to Cox and Moore (1993) "however diverse the habitats that it (herein the island) offers, the variety of the island life depends, in the short term, very much upon the rate at which colonizing animals and plants arrive. This, in turn, depends largely upon how far the island is from the source of its colonizers, and upon the richness of that source. If the source is close, and if its biota is rich, then the island in its turn will have a richer biota than another, similar island which is more isolated or which depends upon a source with a more restricted variety of animals and plants. Each sea barrier further reduces the biota of the next island, which in turn becomes a poorer source for the next." Based on this citation, we can conclude that the isolation and richness of the source population are very important factors in this relationship.

Another concept that has been associated with the distribution of organisms is the nestedness. "The nested subset hypothesis was formulated to describe and explain patterns in the community structure of insular mammals which are in the state of 'relaxation'. The hypothesis states that the species comprising a less species rich fauna should constitute a proper subset of the species in richer faunas, and that an archipelago of such faunas arranged by species richness should present a nested series" (Patterson and Atmar 1986).

In simple language the nested hypothesis assumes that if we have a set of replicate habitats containing faunas of different species richness, less species-rich faunas tend to be subsets of more species-rich faunas. This means that in a perfectly nested subsets, a species present in a given fauna should also be present in all more species-rich faunas. Vice-versa, if a species is absent from a fauna, it should also be missing from all less species-rich faunas. Extinction is believed to play a major role in producing the observed nested substructures; consequently insight into the nested pattern within an archipelago has the potential to reconstruct the faunal extinction sequence and to predict vulnerability of species to forthcoming extinctions (Cutler 1991b, Wright *et al*. 1998) cited in Krystufek and Kletecki (2007).

Mammals have been found to show a pattern were small mammals on the mainland tend to be big on islands while big mammals on the mainland have been found to be smaller on the islands, a pattern that is credited to Fosters work. Foster (1963, 1964, 1965) observed that there is a clear tendency for gigantism in insular rodents and perhaps marsupials, while dwarfism is characteristic of insular carnivores, lagomorphs, and artiodactyls. He further observed that insectivores do not exhibit any clear pattern of insular body size. Van Valen called this phenomenon the ‘island rule’ and described it as “one with fewer exceptions than any other ecotypic rule in nature” (Van Valen 1973). Lawlor (1982) questioned the validity of this rule by suggesting that lagomorphs and heteromyid rodents do not exhibit the predicted trends in insular body size. However, others like Heaney (1978) re-emphasized (even though implicitly) taxonomic differences and interpreted the island rule in more general terms; that is gigantism in the smaller species and dwarfism in the larger species (Foster 1963, 1964, 1965, Heaney 1978, Lawlor 1982) all cited by Lomolino (1985b).

Recently Meiri *et al* (2008) reviewed the island rule and showed there is little support of the rule when phylogenetic comparative methods are applied to a large, high quality data set and thus questioned the generality of the island rule. However, all researchers point out that murid rodents usually comply with the island rule without exceptions. In addition, despite this debate about the validity of the island rule and some evidence that questions the generality of this rule (Meiri and Dayan 2003, Meiri *et al*. 2004a, b, 2006, Meiri *et al*. 2008), this rule has been found to be applicable to other taxa, regions and ecosystems, including reptiles (Case and Schwaner 1993, Petren and Case 1997, Boback 2003, Boback and Guyer 2003), deep sea gastropods (McClain *et al*. 2006), and mammals inhabiting anthropogenically fragmented forests in Denmark (Schmidt and Jensen 2003, Schmidt and Jensen's 2005), volat mammals (bats) (Jacobs 1996, Juste *et al*. 2007, Taylor *et al*. 2012) and some references given in Lomolino *et al*. (2006b). In my opinion, these differences in interpretation of the island rule arise from different researchers using different variables, the inclusion of very big islands and sometimes parts of mainland and also the use of multiple t-test analysis when assessing the validity of this rule. Hence, an agreement of the variables to use when assessing this rule and also trying to find the approximate size of island for which the island rule holds for particular taxa would be a step in the right direction for assessing the validity of the island rule.

Heaney (1978) further explained the factors that are important for the island rule and concluded that "predation, food limitation, interspecific competition, and selection for physiological efficiency, are thought to be major factors in determining the body size of these squirrels and other mammals. Each of these factors is thought to be related to island area and to be of varying importance on different size of islands". More details can be found from and the literature he cited especially Van Valen (1973) and Foster (1965). Lastly, more exhaustive explanation of the causes of the island rule can be found in Lomolino *et al.* (2006a).

3. CURRENT KNOWLEDGE OF MURID RODENTS IN TARUTAO NATIONAL PARK

Focusing on Tarutao National Park, Miller Jr. in 1900 reported the specimens collected by Dr. W. L. Abbott in 1899 while he explored Langkawi and Butang islands. Dr. Abbott collected about 80 specimens comprising 13 species and deposited these in the United States National Museum. (Miller 1900) examined fifteen specimens of *M. surifer*, twelve from Adang and three from Rawi and gave the description of these specimens and he felt these were different from the mainland forms and hence called them as *M. surifer butangensis*. He also examined and described ten specimens of *Rattus tanezumi*, ten from Adang and three from Rawi islands calling the specimens from Adang as *R. rattus pannosus*, and those from Rawi as *R. rattus pannellus*. He also examined one specimen of *Niviventer cremoriventer* from Adang Island. Miller (1900) also referred to *surifer* rats from Tarutao Island as *Mus surifer flavidulus* a name which was also retained by Chasen (1940) but later changed by Hill (1960) to *R. surifer surifer* X butangesis as he felt that this was different from the specimens that were to as *flavidulus* also and he felt that the specimens from Tarutao Islands were probably an intermediate between *R. s. surifer* and *R. s. butangensis* that he thought required sub specific separation from both forms but he could not do this because he had few specimens *R. s. butangensis*.

The second record of murid rodents from Tarutao National Park was given by Thomas and Wroughton (1909). They gave the first description of *L. sabanus* from Tarutao Island referring them a*s Mus vociferans tarsus*, subsp. n.

Then followed Chasen (1940) who referred to the series of *R. tiomanicus* from Tarutao Islands as *R. rattus viclana*, however, this name was later changed to *R. rattus terutavensis* subsp. nov. by Hill (1960) when he observed that the series from Tarutao was different from those which were called *R. rattus viclana* from Langkawi Island.

Records of murid rodents from Tarutao National Park are also found in Gyldenstolpe (1919), Corbet and Hill (1992) however these publications in all cases refer to the specimens used by Miller (1900), Thomas and Wroughton (1909), Chasen (1940) and Hill (1960).

McNeely and Lekagul (1988) did not mention any murid rodent that is found in Tarutao National Park despite having mentioned some other rodents such as squirrels found in Tarutao National Park. The squirrels listed by these authors included; *Ratufa bicolor fretensis* (Thomas and Wroughton, 1909); *Calloscuires caniceps adangensis* (Miller 1903); *Petaurista petaurista* (Pallas 1766); *Petaurista petaurista terutaus (*Lyon 1907) which is the synonym *Petaurista terutaus* (Lyon 1907); and *Hylopetes platyurus* (Jentink 1890) which is the synonym of *Sciuropterus platyurus* Jentink, 1890; and *Hylopetes Lepidus* (Hill 1960) (McNeely and Lekagul 1988).

Meijaard (2003) in his journal article on Mammals of Southeast Asian islands and their Late Pleistocene environments, reported two murids from Tarutao – *L. sabanus* and *N. cremoriventer* – and just one murid rodent from Rawi – *M. surifer* – while none was reported for Adang island. However this list by Meijaard (2003) may be considered as not being an exhaustive account of the murid rodents in Tarutao National Park because in his analysis he did not consider the mammals species which he thought were more likely introduced on the islands in the region and of those he left out in his analysis were some murids including *Bandicota indica, Mus musculus,* *Rattus argentiventer, R. exulans, R. norvigicus and R. tiomanicus* of which he did not indicate on which islands these species where present.

Based on this account, it can be concluded that the islands west of Peninsular Thailand seem not to be sufficiently studied to assess their compositions of mammals. The situation which was pointed out by Glydenstolpe (1919), when he said, “the mammal fauna of Thailand had swollen to a total of three hundred and four species and subspecies, but of those nearly sixty were island races, found exclusively on the islands of Salanga (Puket), Tarutao, Adang, Rawi, etc., off the western coast of peninsular Thailand, and on others situated in the gulf of Thailand. He further said that quite a number of small islands along the western coast of peninsular Thailand have not been visited and explored zoologically up to the time he was writing, and on those several new insular races would most certainly be obtained if the localities were found worthwhile to be visited by a trained naturalist.”

Therefore, some questions that remain to be answered include; how many species of murids are currently found in Tarutao National Park? Are there any differences between the murids on Tarutao, Adang, Rawi, Butong and Yang islands which are the major/larger islands comprising Tarutao National Park and also between these island populations and their mainland relatives/populations? Therefore this research will be conducted with the objective to assess the diversity of murids in Tarutao National Park, a marine national park located on the western coast of Southern Thailand and also to investigate if there any morphological, morphometric or genetic differences of the murid rodents within the National Park and between the island and mainland populations.

4. GENERAL DESCRIPTION OF THE MURID RODENT SPECIES RECORDED IN TARUTAO NATIONAL PARK.

***Maxomys surifer* (common name: red spiny rat)**

M. surfer is a medium sized rat (McNeely and Lekagul 1988, Chaimanee 1998). The dorsal pelage has dark spines and orange/reddish-brown in color with mixtures of black on upperparts and sharply demarcated from the creamy/pure white under parts. Tail about as long as head and body length, bicolored, white below, brown/blackish above but becoming all white more or less half way along the length of the tail with the tip being entirely white (McNeely and Lekagul 1988, Lunde and Son 2001, Francis 2008, Smith and Yan 2008) as can be seen in figure 6. Hind foot elongated and slender (Lunde and Son 2001, Francis 2008, Smith and Yan 2008), nearly five times as long as wide, dorsal surfaces of feet white or pale brown (Lunde and Son 2001), with relatively small footpads, smooth and not well adapted for climbing (Francis 2008) but well-adapted for running on the ground (Chaimanee 1998).

Figure 6; Photos of typical M. surifer taken from Tarutao Island.

Females with four pairs (2 + 2) of mammae; (one pectoral pair, one postaxillary pair, and two inguinal pairs) (Lunde and Son 2001). In terms of its ecology and habitat, this species is nocturnal and mostly terrestrial, living in burrows in primary and secondary forests, and also found in rice fields and gardens, especially if the gardens are adjacent to forests, but not in heavily disturbed areas (Corbet and Hill 1992, Francis 2008), and has never been found in trees and it’s not commensal (McNeely and Lekagul 1988, Chaimanee 1998).

In the skull, squamosal roots of zygomatic arches are set high on the side of the braincase; incisive foramina short and wide, ending well in front of the first molars; posterior margin of palate at level of posterior margin of the third upper molars; mesopterygoid fossa about as wide as palate; bullae relatively small (Lunde and Son 2001, Smith and Yan 2008); pterygoid fossa not perforated by foramina; dentary with small coronoid process (Lunde and Son 2001). The braincase is relatively broad with an elongate rostrum. For the teeth, the upper and lower incisors are orange in color and the molars relatively wide (Francis 2008).

In terms of conservation status, *M. surifer* is recorded as least concern and the population trend is decreasing (IUCN 2011)

Rattus tanezumi **(common name: Asian/Oriental house rat)**

R. tanezumi is a sister taxon of *R. rattus* (commonly called the European house rat) (Lunde and Son 2001, Francis 2008) and this was initially confused with the later species but recently studies now confirm that the Asian form is different from the European form based on both chromosome count and genetic evidence (Francis 2008, Pagés *et al*. 2010).

This is a medium sized rat and adaptable in various habitats including man-made habitats and in urban areas. The fur on the upperparts (dorsum) is olive-brown becoming lighter towards the ventral sides and becoming completely creamy white or buffy-brown on the ventrum. The dorsal fur also has long black guard hairs especially towards the lower back giving it a moderately spiny when you push the fur from the lower back towards the head. The tail is mostly equal to the head and body length and very dark above and nearly lacking hairs on along its whole length. The ears are large and hairless. The feet are well adapted for running and climbing. The Mammae is usually 2 + 3 (McNeely and Lekagul 1988, Corbet and Hill 1992, Lunde and Son 2001, Musser and Carleton 2005, Francis 2008)

Figure 7. Photography of *R. tanezumi* (http://www.ecologyasia.com/verts/mammals/asian-house-rat.htm).

According to Musser and Carleton (2005) is native to Southeast Asia, with the distribution ranging from eastern Afghanistan, through central and southern Nepal (below about 2000m), Bhutan, northern India, northern Bangladesh and northeastern India to southern and central China (including Hainan island), Korea, and mainland Indochina (including offshore islands) south of the Isthmus of Kra but absent on the Andaman islands and most of Nicobar islands although probably native to Mergui archipelago too. This species is thought be a complex of similar species and thus more studies to review the taxonomic status of the populations currently included under this species is recommended by Heaney and Molur (2008).

In terms of conservation status, *R. tanezumi* is recorded as least concern version 3.1 and the population trend is increasing with no major threats (IUCN 2013).

***Leopoldamys sabanus* (common name: Indomalayan Leopoldamys)**

This is a large rat with tail longer than combined length of head and body, sleek smooth fur, guard hairs only slightly longer than rest of fur, numerous spines that are soft and hair like. The tail is not sharply bicolored, however, dorsal surface of tail brown, sometimes mottled brown and white towards the tip, ventral surface of tail pale brown or white (Lunde and Son 2001, Francis 2008). Dorsum reddish brown to grayish brown while ventrum is white to creamy white, sharply demarcated from dorsum. Hind foot long and slender, each with six plantar pads, front and hind feet with broad brown stripes on dorsal surface (figure 8). Females with four pairs of mammae; (one pectoral pair, one postaxillary pair, and two inguinal pairs (Lunde and Son 2001).

Figure 8. Photography of *L. sabanus* (http://chm-thai.onep.go.th/chm/Dry/bdd_animal09.html).

In terms of conservation status, this species is recorded as least concern. However, it’s population trend is unknown (IUCN 2011).

In terms of habitat, this species is common terrestrial rat found mainly on the ground and in lower parts of trees. They have been recorded in tall and secondary forests, but mainly found in lowlands up to 1,200 m in Peninsular Malaysia (Lunde and Son 2001, Francis 2008).

***Niviventer cremoriventer* (common name: Sundaic arboreal Niviventer)**

This is a medium-sized arboreal rat (Lunde and Son 2001, Smith and Yan 2008). The color of the fur on the dorsum is orange-brown to reddish-brown. The dorsum is sharply demarcated white or creamy colored ventral pelage (Lunde and Son

2001, Francis 2008, Smith and Yan 2008) but in preserved animals white may discolor to bright yellow or sulfur yellow, especially when in contact with formalin (Lunde and Son 2001, Francis 2008). According to (Francis 2008), fur varies in texture from soft to semi-spiny, sometimes in the same species, and varies in length from short to moderately long; guard hairs moderately long and conspicuous in some species, inconspicuous in others. Tail usually at least 125% of the head and body length with longer hairs at tip forming a slight tuft (Francis 2008). The tail is usually bicolored (Lunde and Son 2001, Francis 2008, Smith and Yan 2008) dark above, pale below (Lunde and Son 2001) but in some specimens it may be monocolored (Smith and Yan 2008). Hind feet are relatively short and broad and have six well-developed large plantar pads for climbing (Lunde and Son 2001, Francis 2008) (figure 9).

Adult females with four (2 + 2) pairs of mammae (one pectoral pair, one postaxillary, and two inguinal pairs) (Lunde and Son 2001, Francis 2008, Smith and Yan 2008), but some species may sometimes have 1 + 2 (Francis 2008).

This species is active at night. It is a good climber in small trees, lianas and shrubs and it is also active on the ground. It has been recorded in a variety of habitats from forest edges, tall and secondary forests, lightly wooded areas from near sea level to 1,900m. it’s diet is mainly composed of plant matter, including fruits and seeds, but they also consume insects (Lunde and Son 2001, Francis 2008).

Figure 9. Photography of *N. cremoriventer* (http://www.arkive.org/sundaic-arboreal-niviventer/niviventer-cremoriventer/image-G86715.html).

In terms of conservation status, *N. cremoriventer* is denoted as vulnerable A2c and its population trend is decreasing (IUCN 2011).

According to (Francis 2008), taxonomy of this species (including other species in this genus) is still somewhat uncertain; some species occurring north of peninsular Thailand can be difficult to identify. This therefore, would suggest that more research should be done in this genus to clearly distinguish the species in the northern peninsular of Thailand. This can be done by using more morphological, cranial and DNA data.

***Rattus tiomanicus* (common name: Malaysian wood/field rat)**

This is a medium sized rat and very similar to *R. tanezumi* with only a few differences in external morphology making it difficult to differentiate between the two species in the field especially juveniles. However, unlike the later species, in *R. tiomanicus* the dorsal pelage is sleeker with guard hairs scarcely protruding beyond contour hairs (Corbet and Hill 1992). The ventral pelage is usually pure white (Corbet and Hill 1992, Francis 2008) (figure 10). The tail is entirely dark brown and hairless. The ears are large and thinly furred. Adult females have a mammae formula of 2 + 3 (Francis, 2008)

Figure 10. Photo of *R. tiomanicus* (http://www.ecologyasia.com/verts/mammals/malaysian_wood_rat.htm).

This is a nocturnal rat occurring mainly in scrub, gardens, secondary and coastal forests, plantations (such as oil palm), and grasslands (Corbet & Hill, 1992; Francis, 2008). This species is rarely captured in dipterocarp forests and not known to enter houses (Francis, 2008). However, it has the potential to be found in houses in the absence of *R. tanezumi* and also in undisturbed forests on islands where indigenous forest rats are absent (Corbet & Hill, 1992)

In terms of diet, these rats are omnivorous, eating a wide variety of plant (including oil palm fruits) and animal matter, and highly adaptable (Francis 2008, Smith and Yan 2008).

In terms of conservation status, *R. tiomanicus* is classified as least concern and the population trend is increasing probably owing to the fact that it is widely distributed (IUCN, 2011).

5. GEOGRAPHICAL LOCATION OF TARUTAO NATIONAL PARK

Thailand lies within two major biogeographical regions, the Indochinese region in the north and the Sundaic region in the south (Pookpakdi 2000), and does not have any distinctive floristic elements as the majority of its flora and fauna are closely related to those in neighboring countries, thus it can be considered as a collective center of biological diversity (Bugna and Rambaldi 2001). Boonsong *et al*. (1998) further divided Thailand into four regions as northern, northeastern, central and southern regions. Others however, divide Thailand into six regions (Pookpakdi 2000). This study was conducted in Tarutao National Park which is located off the western coast of southern Thailand.

"Tarutao National Park is located in the Andaman Sea off the west coast of peninsular Thailand in Satun Province between 6° 30´ N and 6° 44´ N latitude and 99° 44´ E and 99° 9´ E longitude" (Congdon 1982).Tarutao National Park was gazetted as a National Park on 19th April, 1974. It has an area of 1,490 square kilometers and is described as a coastal and marine ecosystem, IUCN category II (UNDP undated). Tarutao National Park was declared as an ASEAN Heritage National Park on 29th November 1984 at a meeting held by ministers for the environment in Bangkok (ASEAN 1984). With its wide variety of marine and terrestrial ecosystems offering outstanding scientific value, as well as its exceptional natural beauty, Tarutao National Park was nominated as a World Heritage Site in 1990. But problems with illegal dynamite fishing and trawling that had severely damaged reefs, plus the drastic loss of nesting turtles, kept Tarutao from meeting the criteria for inclusion under the category of natural property, and the area ultimately was not recommended (Wongbusarakum 2007). Tarutao Marine national Park is one of the most exquisite and unspoiled regions in Thailand. It encompasses 51 islands covered with well-preserved virgin rainforest teeming with fauna, as well as sparkling coral reefs and radiant beaches. This national park is protected partly by its national park status, and mostly by its relative inaccessibility (Williams *et al*. 2007). The islands in Tarutao National Park are considered as one of the important sites for birds (Pookpakdi 2000).

Wongbusarakum (2007) further elaborates that this area has a tropical monsoon climate, affected by the northeast (dry) and southwest (wet) monsoons. The rainy season runs from May through to October, when the southwest monsoons bring rain from the Indian Ocean. During the dry season, November to April, when the northeast monsoon prevails, the climate is suitable for tourism. The hottest time of the year is March and April, when the monsoon winds change direction. The average year-round temperature is 27.74˚C, from a high of 32.44˚C in March to a low of 23.74˚C in February. The average relative humidity in Satun is 77.86 percent, highest in October (84.22 percent) and lowest in February (66.52 percent).

Geologically the Islands in Tarutao National Park are part of the Sunda Shelf. They were formerly hills on dry land which was connected to the mainland. However, due to the rising seas fed by melting ice caps cut them off from the mainland about 8,500 years ago (Wongbusarakum 2007) a view supported by the sea water level maps of the Pleistocene and Holocene showing the transgressions and submerged lakes on the Sunda Shelf between 10.88 Ka BP and 8.38 Ka BP (figures 11 A and B) repectively (Voris 2000, Sathiamurthy and Voris 2006).

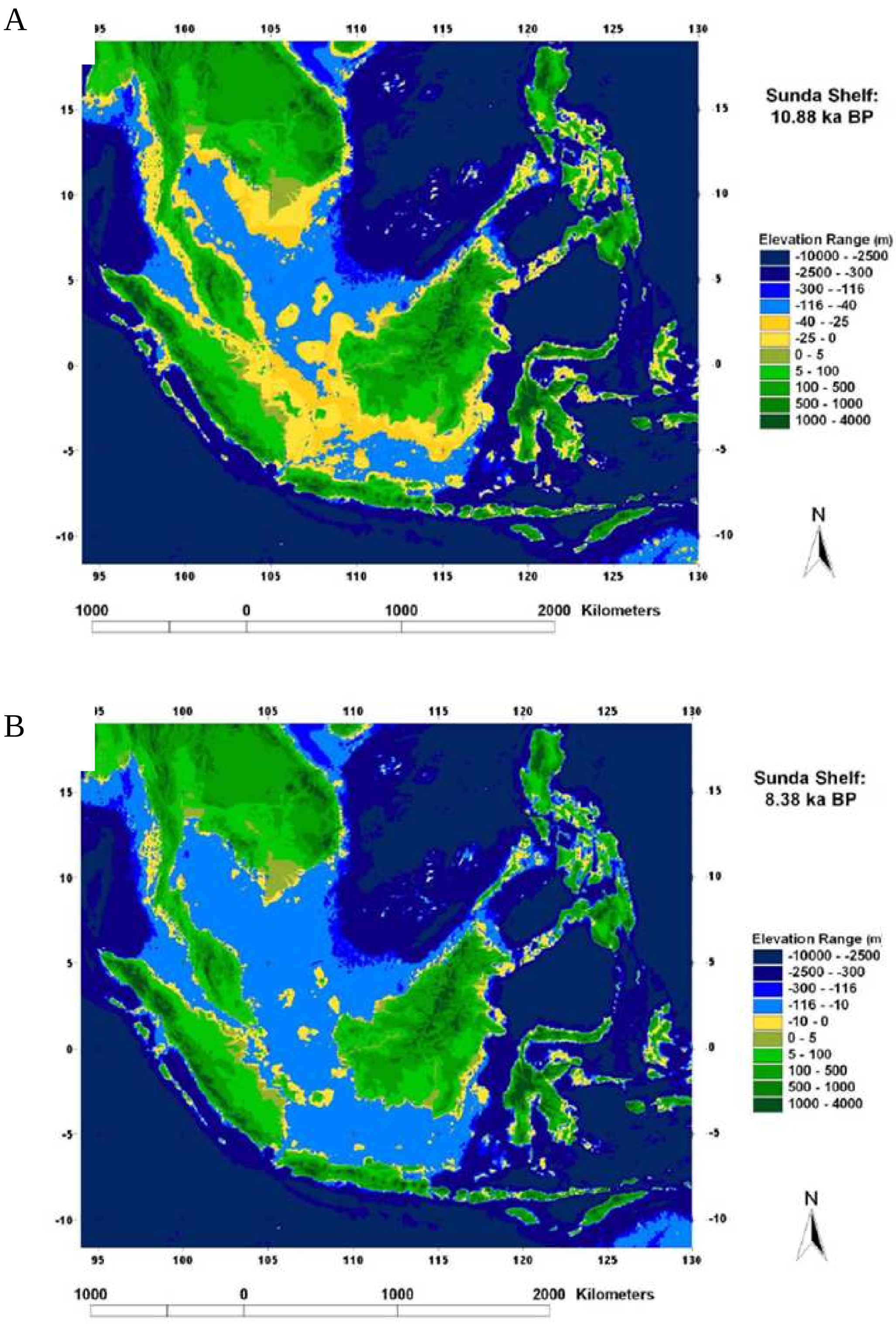

Figure 11: Maps showing the sea level changes in the Sunda Shelf between (A) 10.88 Ka BP and (B) 8.38 Ka BP (based on and modified from Sathiamurthy & Voris, 2006).

CHAPTER 3

DIVERSITY AND DISTRIBUTION OF MURID RODENTS ON FIVE ISLANDS IN TARUTAO NATIONAL PARK

INTRODUCTION

Tarutao National Park is located off the western coast of Thailand and it is composed of 51 islands. These islands were once part of the mainland, the presence of murid rodents on these islands can be either before or after these islands had separated from the mainland (with the mainland acting as the source population). Hence based on the equilibrium model of island biogeography by MacArthur and Wilson (Lomolino *et al*. 2006a) these islands initially had unbalanced faunas which after time relaxed to equilibrium. If this is the case, then it is safe to assume that these islands were formed as a result of fragmentation from a continuous mainland habitat which supported common species pool prior to the rise in sea water levels and thus the murid rodents on these islands would be composed of non-random subpopulations of the total available species pool on the mainland (Cutler 1991a). Although it is unknown how many times that these Islands have been isolated from the mainland, the latest isolation is approximately 8,500 years ago (Wongbusarakum, 2007).

This National Park become an ASEAN Heritage National Park in 1984 and has received very little attention with regards to the study of murid rodents for more than 100 years despite some studies in plants (Congdon 1982, Chantanaorrapint 2010), social welfare of the local people in the National Park (Wongbusarakum 2007), a number of studies on ants (Watanasit *et al*. 2003, Watanasit and Jantarit 2006, Abdullah and Watanasit 2011) and recently in bats and birds (by researchers from Prince of Songkhla University but not yet published) being conducted in the National Park. However, despite murid rodents being important as seed dispersers, in zoonoses and other ecological functions, there has been no comprehensive and exhaustive study of them in this National Park. The main focus of the section is to understand the distribution pattern of the murid rodents on the islands in this National Park. The distribution patterns were assessed by applying the species-area relationship, species-isolation relationship and nestedness.

The species-area relationship is one of community ecology's laws (Schoener, 1976) and one of the most general, best documented patterns in nature (Lomolino, *et al*. 2006). This is a relationship in which the species richness tends to increase with increasing area. Since the areas of the five islands from Tarutao National Park included in this study varied in size we assessed the strength of the island area has on the species richness of murid rodents.

The species-isolation relationship is also one of the well studied patterns in nature. According to Lomolino *et al*. (2006) "since the early 1800s, it has been well known that single, isolated islands far out in the ocean support fewer species than islands that are part of a major archipelagoes or islands that are located nearer to continents. Therefore, for a variety of taxa and ecosystems, species richness should decline as a negative exponential or sigmoidal function of isolation." Despite having the knowledge that the isolation of four islands included in this study are not very different we still tested this relationship.

Suffice to say that past records of murid rodents in Tarutao National Park have exclusively been to identify the murid rodents based on collections of museum specimens (Miller, 1900; Thomas and Wroughton, 1909; Chasen, 1940). Therefore, very little is known about the biogeographic distributions of the murid rodents around the small islands in South East Asia and also in Tarutao Nation Park. This evident from the study of Meijaard (2003) who in his analyses excluded the specimens from Tarutao National Park on the basis that there was little information of the murid rodents from this site. Here we attempted to apply some biogeographic theories of the species-area, species-isolation and nestedness distribution of the murid species in Tarutao National Park in basic sense. Therefore, in this chapter, we do not go into details of using the various formulas but the analysis of the discussions were based on the capture of the murid rodent in this study.

Another trend that has been observed in a number of insular taxa is the nestedness pattern. “The nested subset hypothesis was formulated to describe and explain patterns in the community structure of insular mammals which are in the state of ‘relaxation’. The hypothesis states that the species comprising a less species rich fauna should constitute a proper subset of the species in richer faunas, and that an archipelago of such faunas arranged by species richness should present a nested series” (Patterson and Atmar 1986). This means that a less rich fauna will represent a subset of the more species rich faunas and if a species is absent in the species-rich fauna then it should also be absent in the less species-rich fauna if the distribution represents a perfect nested subsets provided they have the same source populations (mostly considered to be the mainland or nearest major island).

All these three trends discussed above are believed to be basically driven by immigration and extinction leading to the population reaching relaxation in distribution. The aim of this section was to assess these biogeographic theories using murid rodents from Tarutao National Park as models by consulting both museum collections and also conducting extensive field trappings. In the process this study will also help to update the knowledge of the murid rodents currently present in the National Park and provide the understanding of how they are distributed.

MATERIALS AND METHODS

Study areas

Tarutao National Park is located in the Andaman Sea off the west coast of peninsular Thailand in Satun Province between 6° 30´ N and 6° 44´ N latitude and 99° 44´ E and 99° 9´ E longitude (Congdon 1982). It was gazetted as a National Park in 1974, covers an area of 1,490 km^2 and is described as a coastal and marine ecosystem, IUCN category II (UNDP undated). In 1984 Tarutao National was declared as an ASEAN Heritage National Park (ASEAN 1984). Tarutao National Park encompasses 51 islands covered with well-preserved virgin rainforest which have a rich fauna. Most of these islands are considered important sites for birds (Pookpakdi 2000)

This study was conducted on five islands in Tarutao National Park namely; Tarutao, Adang, Rawi, Butong and Yang (or Ka ta) islands (figure 12). The size of these islands ranges from <1 km^2 (Yang Island) to as large as 151 km^2 (Tarutao Island). The various dimensions of the islands included in this study are summarized in table 1.

Table 1: The Islands in Tarutao National Park included showing the length, width, highest point and area (based on and modified from: Wongbusarakum, 2007: 80). The relative distance from the mainland and the dimensions Yang estimated from Google Earth.

Island	Length (Km)	Width (Km)	Highest point (m)	Area (Km^2)	Relative distance from mainland (km)
Tarutao	26.5	11	712	151	26
Adang	8.7	5.1	695	29.8	~71
Rawi	10.6	5	481	28	~82
Butong	3.5	2.8	265	4	~90
Yang	~0.91	~0.46	-	<1	~76

The largest island is called **Tarutao Island:** (or Koh Tarutao by the local people) and this is home to the park headquarters and government accommodation. Tarutao Island covers about 151 square km and it is covered in dense, old grown jungle that rises sharply up to the park’s 713 m peak (Williams *et al.* 2007). Tarutao Island lies approximately 26 km off the mainland of peninsular Thailand and 10 km due north of Malaysia’s Langkawi Islands at its southernmost tip. The topography of the island is dominated by mountain ranges running from north to south and between these ranges are low valleys where streams flow throughout the year. The west coast of the island is characterized by long sandy beaches, mangrove swamps, and densely forested hillsides descending to the sea while the east coast consists of craggy limestone rocks, small islands, and scattered small pockets of mangrove swamp (Congdon 1982).

Adang which is the second biggest after Tarutao Island is a mountainous island that reaches nearly 700 meters at its highest point. Most of this island is covered by thick evergreen and deciduous forest, which includes many edible and herbal plants. Sources of fresh water on this island are numerous including rivers, streams, waterfalls, and ponds. It also has few flat areas of fertile land by the sea to cultivate crops and fruit trees. Small white-sandy beaches and bays are a common feature along the coastline except for small stretches on the very northwestern tip, which are rocky. The island also has healthy coral reefs (Williams *et al*. 2007, Wongbusarakum 2007)

Rawi is located 11 km west of Adang Island. As the case with Adang, this island is mountainous, with rich evergreen and deciduous forest. The mountains peaks are slightly lower than on Adang Island with a few mountain peaks in the middle of the island ranging from 301 to 481meters, and the highest peaks are to the east. The south and north sides of the island have many freshwater sources, including waterfalls, streams, ponds, and swamps, some of which dry up during the dry season. There are many patches of mangrove along the south shore. On the west there are long stretches of rocky coastline with the northwestern side being rocky and has a large waterfall (Williams *et al*. 2007, Wongbusarakum 2007).

Butong is situated close to the western end of Rawi Island. This island also has a forest more similar to the other islands but it is drier. One site was sampled on this island near a stream on the northern west end of the island.

Yang or **Ka Ta** was the smallest of the island included in our study and it is located between the islands of Adang and Rawi. This island is not very high and has a lot of fresh water sources around the island.

The descriptions of Butong and Yang Islands are based on personal observations when conducting the field research on these Islands and also from Google map because no literature was found describing the nature of these islands.

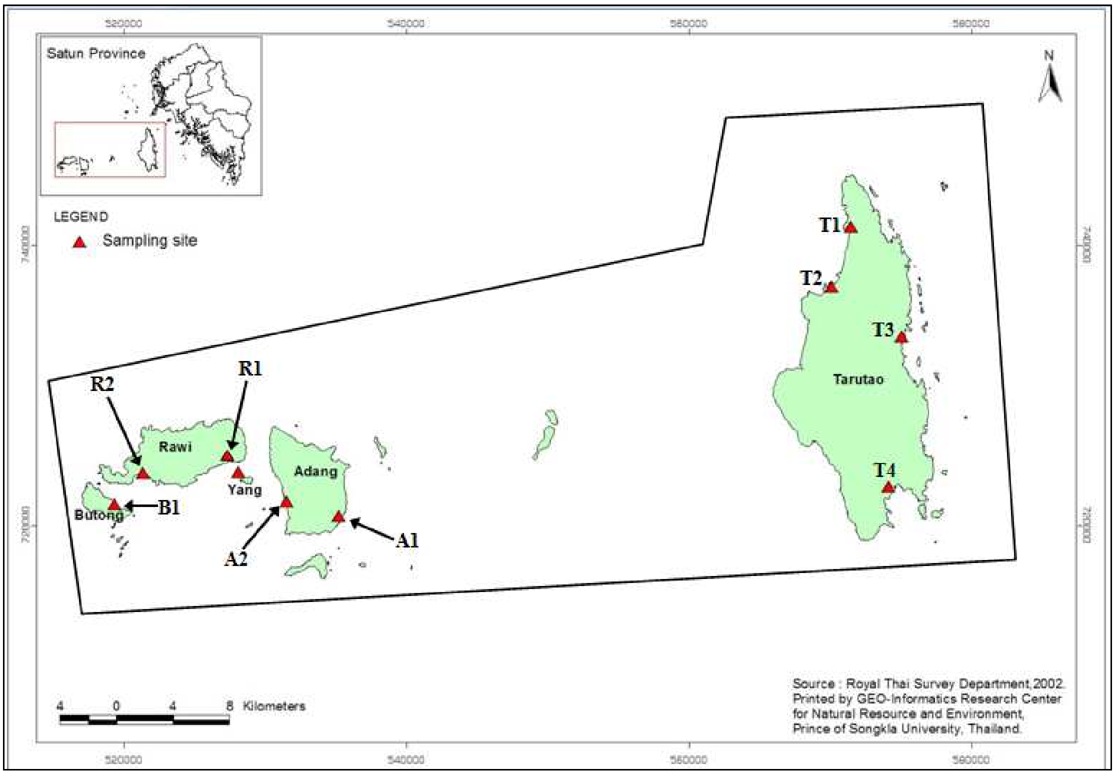

Figure 12: Map of Tarutao National Park. The labels T1, T2, T3 and T4 show the sampling sites on Tarutao Island, A1 and A2 are the sampling sites on Adang, R1 and R2 were the sampling sites on Rawi Island, B1 was the only site sampled on Butong and the whole of Yang was sampled.

METHODS

Trapping in the field

For the purpose of assessing the diversity of murid rodents in this study, care was taken not to kill all the animals as this was not the objective of trapping them, but to record their presence in an area and only a few specimens were collected to be sacrificed as museum specimens.

Live murid rodents on five islands were sampled using live cage traps baited with either corn or banana from 11-16th February and 15-20th March 2012 on Adang, Rawi, Butong and Yang islands and from 5-15th January of 2013 on Tarutao Island. At each site 25 traps were set at approximately 40-50m intervals (except for Tarutao island were the traps were spaced for approximately 70-100m intervals considering the size of this island compared to other islands). Further at each site the traps were divided into two sets to try and maximize the area covered (one set had 12 traps and the other 13 traps). The traps were randomly set starting from near the coast (beach) and moving towards the interior of the forest and the distance between the two sets of traps at each site ranged from 200-300 meters to try and increase the area covered.

On Adang, Rawi, Butong and Yang the traps were left at each site for at least three nights and checked once per day in early morning and the bait was replaced/changed at the time of checking. The traps were then moved to new places but within the same site to cover as much microhabitat and area as possible meaning a total of 150 (6 days x 25 traps) trapping nights per site. On Tarutao Island we spent three trapping nights with all the 100 traps at one sampling site per time. We then moved to another sampling site and covered four sampling sites on this Island in total as follows; (1) on the north end we trapped at Phante Malacca and the places near to Phante Malacca; (2) on the west side we sampled at Ao Molae, Ao Sone and along the trail leading to Ludu waterfall; (3) on the eastern end we sampled at Talow Wow and along the trail leading to Taloh Udang; and (4) our last site was at the south end and here we sampled around Taloh Udang and along the trail leading to Taloh Wow. This means on Tarutao Island at each site we had a total of 300 (3 days x 100 traps) trapping nights per station. Each point where the trap was set was marked using a GPS and the figure 13 below shows an example of how the traps were set at each site (Ao Sone site).

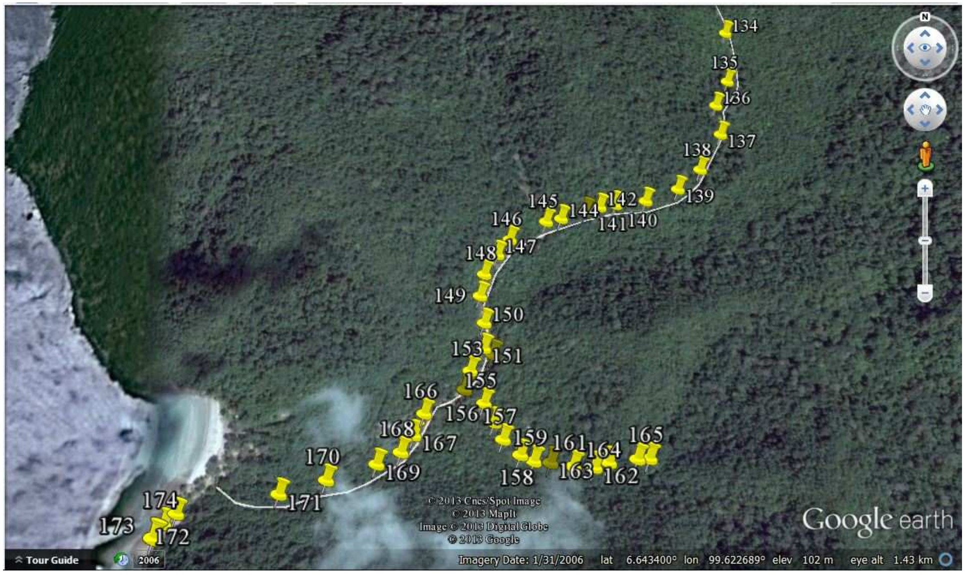

Figure 13: Pictorial view of traps marked using a GPS. This picture shows the setting at Ao Sone (T2 on figure 15) site located on the west of Tarutao Island.

The traps were placed at random to cover different habitats as much as possible with some traps set on the ground with different plant covers, some were set near streams, some on trees/branches and some along fallen dry trees (figure 14).

Figure 14: Photographs of some habitats were the traps set during this study.

The traps were most often baited with banana or corn because these are well known as the baits for trapping rats and also because these were readily available in local markets. The purpose of “the baits are not only to lure rats to the traps, but also to sustain them once they have been caught. The traps were usually visited once a day in the early morning, however, where possible traps were checked twice a day to reduce the stress of capture (Sutherland 2006). However, after our first field study, we decided to use more of corn than banana because of the unwanted trapping of tree shrews which was highly associated with traps in which banana was used as bait. The specimens were identified in the field following the guide book by Francis (2008) and the taxonomy is after Musser and Carleton (2005).

The specimens for collection as voucher specimens were sacrificed using chloroform. The specimen was placed in a container with an air-tight lid containing cotton wool moistened with a few drops of chloroform. However, since chloroform is intensely irritating to the skin and mucous membrane and care was taken not touch neither the mammal nor the biologist. Therefore, when working with chloroform care was taken so that it was not breathed by anyone near or used near an open flame. The specimen was then given a field label and then kept in a cool box containing ice (Sutherland 2000). At least four adult individuals were collected for each species captured, preferably, two males and two females. The other captured individuals were just recorded, measured, sexed, and age determined, and then released at the same point of capture in the field as explained in details in chapter 4.

The species richness and relative abundance for each island was simply established depending on the total number of individuals captured. The distribution of each species was mapped to represent the diversity of the species in the National Park. Further, some biogeographic theories of the species-area and species-isolation relationships, nestedness distribution and island rule were tested in this chapter.

RESULTS

a) DIVERSITY, RELATIVE ABUNDANCE AND DISTRIBUTION OF MURID SPECIES.

The diversities of murid rodent species captured on the five Islands included in this study were 4 species on Tarutao, 3 species on Rawi, 2 species on Adang and 1 species each on Butong and Yang Islands (Table 2). The most common species was *R. tenazumi* which was widespread across all the five Islands, followed by *M. surifer* which was recorded on three Islands (Tarutao, Adang and Rawi) while *N. cremoriventer* was recorded on Tarutao and Rawi islands, finally *L. sabanus* was restricted to Tarutao Island only.

Table 2. The number of murid rodent species captured, the total numbers of individuals and trapping effort (in terms of trapping nights) on each Island during the study period.

	Tarutao	Adang	Rawi	Butong	Yang
No. of species found	4	2	3	1	1
Total number of individuals trapped	97	27	17	3	11
Total trapping nights	1000	600	600	162	126

In terms of the abundance, a total of 155 individuals of 4 murid rodent species were captured, hence, this is the first extensive study of the murid rodents from this National Park based on both the number of islands surveyed and the numbers of individuals captured. *Maxomys surifer* was the most abundant species and representing 48.4% of all the murid rodent species caught, followed closely by *Rattus tanezumi* (41.3%), then *Leopoldamys sabanus* (7.7%) and the remaining 2.6% was accounted for by *Niviventer cremoriventer*.

There was no particular pattern in the distribution of the species composition of murid rodents captured from one site to another on all the Islands (figure 15).

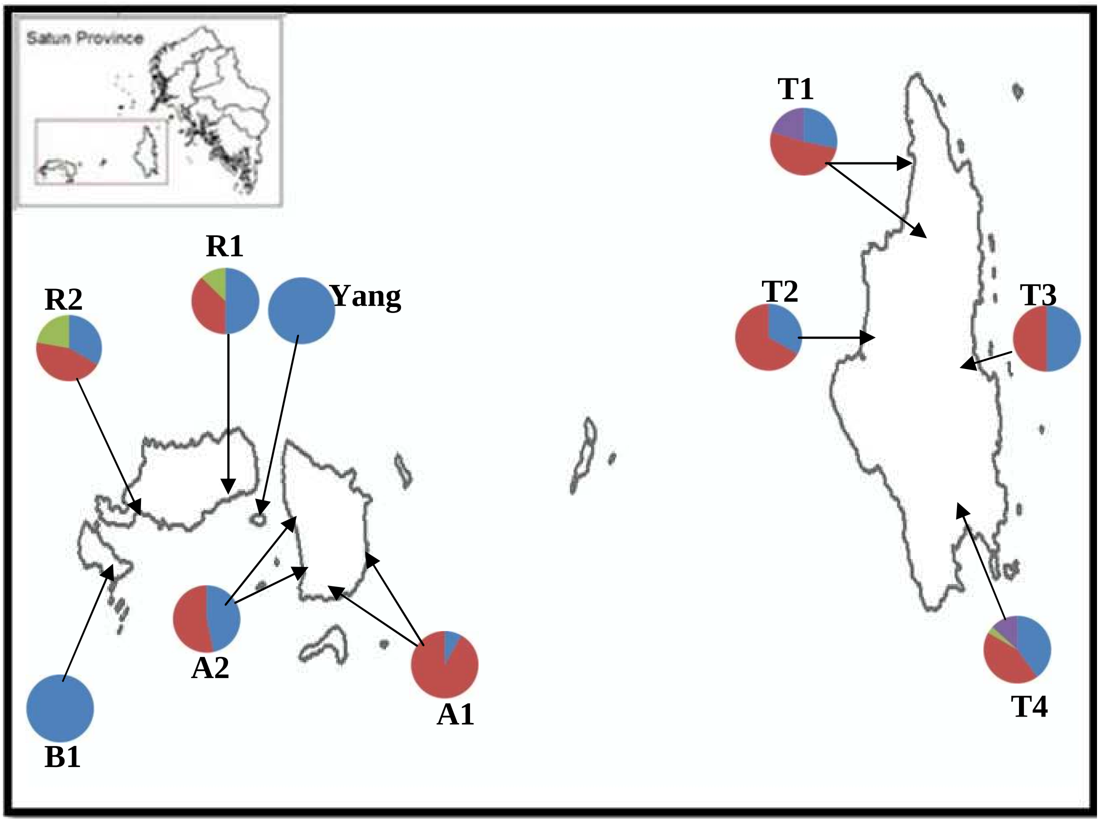

Figure 15. Map of the species richness, relative abundance (represented by the pie chart) and distribution. The colors represent *R. tanezumi* (blue), *M. surifer* (red), *N. cremoriventer* (green) and *L. sabanus* (purple)

b) THE EFFECT OF AREA AND ISOLATION ON THE DIVERSITY OF SPECIES AND THEIR DISTRIBUTION PATTERN.

Our results found that the diversity of species on each Island were greatly influenced by the area and to a less extent by isolation of that Island from the mainland based on the r^2 values, 0.882 for species-area relationship and 0.474 for the species-isolation relationship (figure 16 and 17). Tarutao Island which is the largest (151 km^2) and close to the mainland (26 km away) had the highest number of species and also the densities were high. The other four islands are almost equidistant in terms of isolation from the mainland (70 km from the mainland and 45 km from Tarutao Island). Adang and Rawi are almost equal in area (with 29.8 km^2 and 28 km^2 respectively) and had almost the same number of species, 2 and 3 species respectively but if we put into consideration of the records reported by Miller (1900) we can say that both these island have three species each. Butong is much smaller (only 4 km^2) than Adang and Rawi and had only one species. The smallest island Yang (<1 km^2) also had only one species.

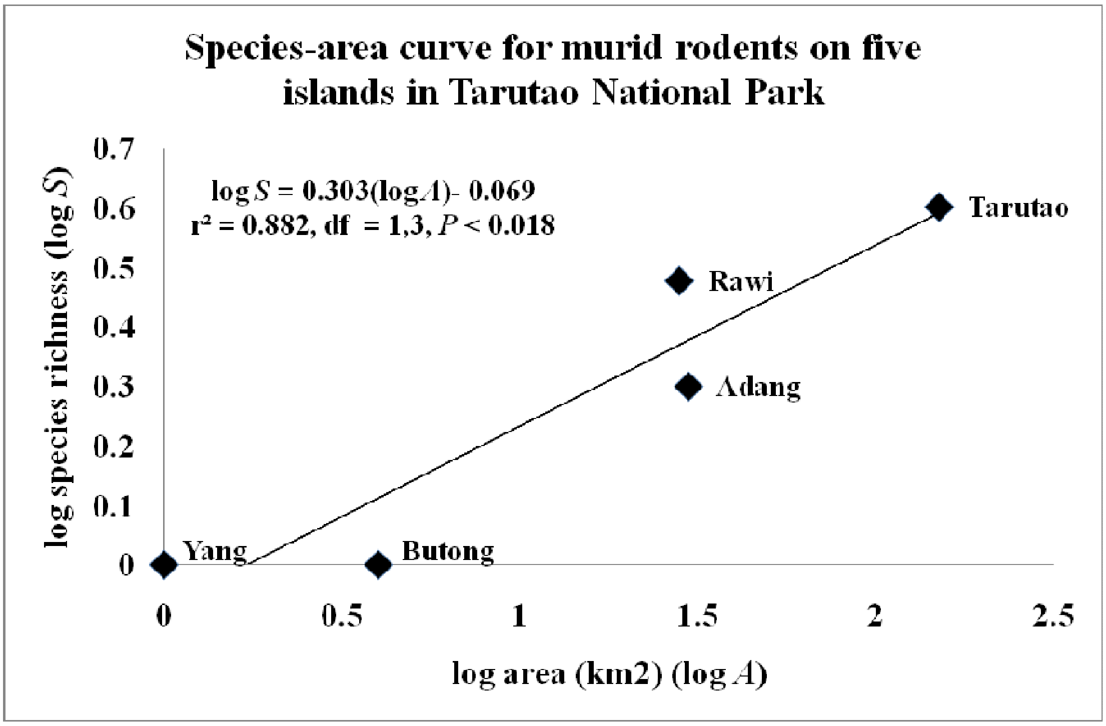

Figure 16. Species-area curve of murid rodents based on the individuals captured in the present study. The graph follows the Arrhenius equation ($\log_{10} S = c + z \log_{10} A$). See text in the introduction for further explanation of the equation.

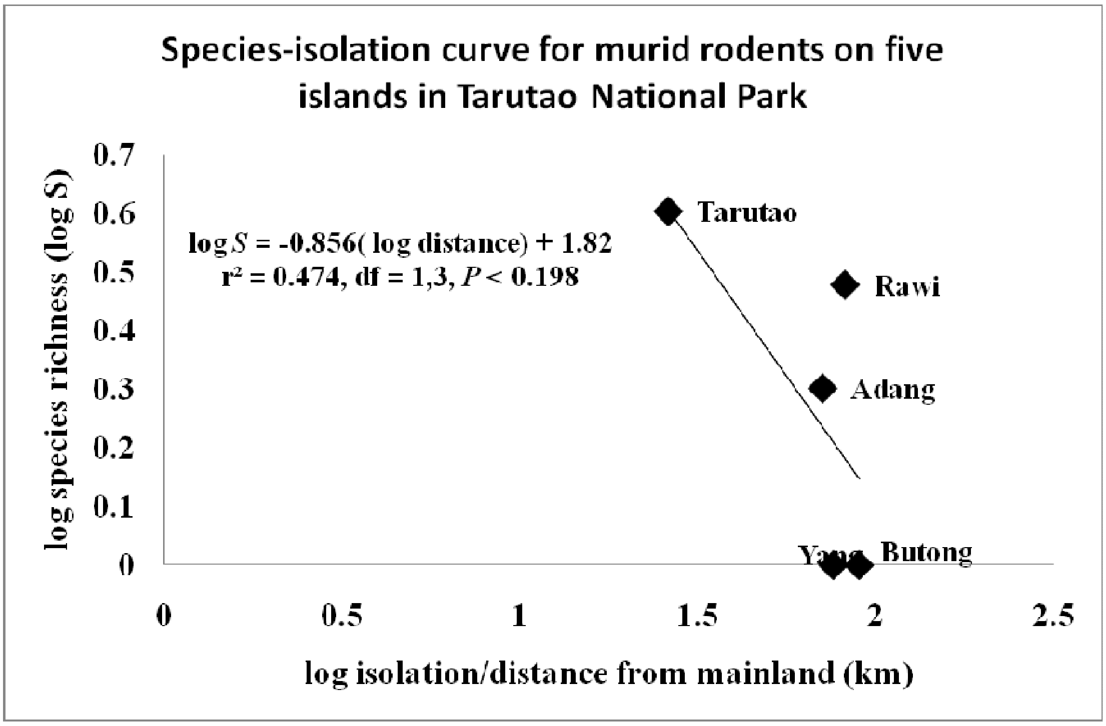

Figure 17. Species-isolation curve of murid rodents based on the individuals captured in the present study.

Despite using a few islands and testing the biogeographic theories in simple terms, our results also show quite a good structure in terms of distribution of the species on the islands in Tarutao National Park as shown in table 3. Our results show that the distribution is thus not by chance or randomly but well structured as would be predicted of a nested distribution. From the table below it can be seen that the species composition on each islands have to do with the area and isolation of that island from the mainland or nearest major island. The results show what would be expected of a fauna in a relaxed state or at equilibrium as would be predicted of a perfectly nested fauna.

Table 3. The presence-absence matrix of species on each island of captured murid rodents. *S* is the total number of species recorded on each island. Species are ordered in such a way with the most widespread first and the least common last.

Species	Tarutao island	Adang island	Rawi island	Butong island	Yang island
R. tanezumi	✓	✓	✓	✓	✓
M. surifer	✓	✓	✓	x	x
N. cremoriventer	✓	x	✓	x	x
L. sabanus	✓	x	x	x	x
S	4	2	3	1	1

DISCUSSION

Despite the first collections of murid rodents in the National Park having been in the late 1800s and early 1900s, the species that we found on the islands are still the same with what was recorded in those collections. This means that the species composition over approximately a period of 100 years has been the same and thus we can assume that the habitats on the Islands of Tarutao National Park have not been disturbed. However, the only slight difference between the earlier records and the current study is that our results for the species richness are not different from what is reported in the literature except that in this study we recorded *N. cremoriventer* on Rawi Island while in the previous collections this species was only recorded on Tarutao and Adang Islands. This difference could be understood because the numbers of individuals of this species captured were very low (with only one individual on Tarutao and three individuals on Rawi). Therefore, it could be a possibility that there is also a small population of *N. cremoriventer* on Adang but we could not capture any individual during our study.

The results showed that *M. surifer* despite being found only on three out the five islands sampled (table 3). This would be explained in terms of island rodents having a tendency to support high densities according to the island syndrome in rodents (Adler and Levins 1994). *R. tanezumi* was the second in terms of the individuals captured and this could be due to the fact that this was wide spread across all the five islands. The widespread distribution of this *R. tanezumi* can be explained from the fact that it is highly adaptability to various habitats, both disturbed, undisturbed and also in human settlements (Francis, 2008; Corbet and Hill, 1992). Another reason could be that *R. tanezumi* is a better colonizer and/or competitor than the other species and in addition to its association with humans has been able to establish itself on all the islands which were included in our study. *R. tanezumi* in particular which is a sister taxon of *R. rattus* (Lunde and Son 2001, Musser and Carleton 2005) is also expected to have the same behavior of territorial defense, generalists in diet (taking almost whatever food is available), known to displace smaller species such as *R. exulans* from their environmental niches and once it establishes itself has shown greater resilience to natural disasters such as short time flooding of an island by storm surges (Spennemann 1997).

On the other hand *L. sabanus* could have invaded Tarutao Island only because this is a bigger island and would provide enough resources and home range for this species and this is probably the reason it restricted itself to the bigger island only. The low density of *N. cremoriventer* could be explained from a point of view of the size of this species. Being the smallest of all the species recorded it could explain why it favored close to the forest edges which were a bit disturbed by humans and not in sympatric with other species may due to competition from the larger species in the interior of the forest.

Another point of interest was that despite Yang being smaller in area than Butong more individuals were captured on this island than the latter despite setting more trapping nights on Butong (27 traps x 6 nights = 162 trap nights) than Yang (21 traps x 6 nights = 126 trap nights) Island. The relative isolation of Butong from Adang and Rawi as compared to Yang islands could help to explain the observed increased density of the individuals on Yang Island as compared to Butong

Island. Therefore, the higher density of *R. tanezumi* individuals on Yang as compared to Butong did not follow the species-area relationship. However, it can be explained in terms of resource availability and proximity to other small Islands. Butong as can be seen on the map (figure 12) is located on the periphery of the other islands. In addition, it has fewer fresh water sources as compared to Yang Island, which lies somewhat between Adang and Rawi and has more fresh water source and also a rubbish pit where tourists dump their left over foods after snorkeling around this small island hence increasing the food resources for the individuals and increase the rate of reproduction.

Even though we conducted the study on only 5 islands, the species – area curve had a high r^2 value (figure 16) an indication that the area of the island has a great effect on the number of species on that island because these islands had different sizes. It is also important to note here that an exception to the species-area relationship called the small island effect (McArthur and Wilson 1967) was found. The small area effect is tendency of species richness varying independently of the island area for smaller island (or biotas) less than 3 acres (Niering 1963) and this varies in a manner consistent with the resource requirement, immigration abilities, and degree of isolation of these biotas (Lomolino and Weiser 2001). Therefore, the islands of Yang and Butong were smaller to conform to the expected species-area relationship.

On the other hand the isolation of the islands seemed not to have a greater effect ($r^2 = 0.474$) (figure 17). This result was not surprising because with the exception of Tarutao Island which had a different distance from the mainland, the other islands are very close to each other and hence they somewhat clumped together on the graph. It is worthy to note here that this does not mean isolation of the Island does not have an effect on the species richness but that the islands included in this study were too close to each other and hence this relationship could not be clearly assessed, thus if one wants to test this relationship, they should ensure that the Islands have varying distances from the mainland or the nearest big island.

From the pattern shown in the distribution of murid rodents in this National Park, it can reasonably be assumed that the species first colonized Tarutao Island from the mainland, which in turn acted as the source population for secondary colonization or dispersal to the other smaller islands which are further from the mainland. Another possible explanation of this pattern observed could be that originally when the Islands were still connected to each other they had the same species but after isolation, on the small Islands there could be competition among the species leading to extinction of less competitive. Our results showed a perfectly nested distribution of the murid rodents on the islands in the National Park associated with the size and isolation which is a characteristic of extinction dominated faunas with no subsequent recolonisations as described by Atmar and Patterson (1993). However it is hard to confidently point out which species are indigenous or introduced to the National Park because there is no fossil records of the original fauna in this National Park, therefore, this distribution can only be associated to isolation/area of the islands and possible extinction of the species.

Despite this being a basic test of the biogeographic theories discussed here, it was evident that various factors could be behind the current distribution patterns of murid rodents on the islands in Tarutao National Park ranging from the which faunas are actually the source populations for these species, what might be happening to the species post-isolation from the mainland more than 8,500 years ago, to extinctions which could result from human caused habitat degradation. However, as pointed out earlier, because lack of supplementary information, it still remains unclear which mechanisms is responsible for the current species composition on the individual islands (Krystufek and Kletecki 2007)

It is worth mentioning here that from our experience in the field during this study, we initially started with corn and banana as baits in our first field trip then in the later field trips we had to depend mostly on corn as the bait. This is because when we used banana and corn as baits we trapped a lot of tree shrew (73 individuals in one week, most likely *Tupai glis*) and we felt this had an effect on the capture of murid rodents. When we used corn alone as the bait, less than 15 individuals (in three weeks period) of tree shrews were caught and the number of murid rodents captured increased. From our results on the effect of baits, it would be advisable to choose the correct and appropriate baits for studying small mammals because the non-target species may come to your traps hence reducing the number of traps open for your target species per trapping night and also sometimes these unwanted species can die in the trap which is not appropriate. Hence bait selection is important to avoid accidental capture of non target species. This view corroborate with the findings of Do *et al*. (2013) and Shonfield *et al*. (2013). This can be achieved by following other studies which specify the specific baits used and minimized accidental captures of non-target species or from a pilot study like in our study.

In conclusion, it can be said that despite this being the most extensive and exhaustive research of murid rodents to be conducted in this National Park, more research would be required especially at the sites where we could not access in this study to come up with a more complete list of the species richness of murid rodents in Tarutao National Park. However, it can also be predicted in simple terms that the species lists for the islands are not likely to change very much because despite visiting multiple sites in our study as shown on the map, the species composition was essentially uniform within the sites on each island.

CHAPTER 4

THE COMPARATIVE PHYLOGEOGRAPHY OF TWO MURID RODENTS (*R. tanezumi*, AND *M. surifer*) FROM TARUTAO NATIONAL PARK

INTRODUCTION

According to the island syndrome, “populations of rodents isolated on islands often show systematic differences in demography, reproduction, behavior, and morphology when compared to mainland populations” (Adler and Levins 1994). The islands that compose Tarutao National Park are part of the Indo-Australian Archipelago (IAA) in a broader scale and confined to the Sundaland region in particular (Lohman *et al*. 2011). However despite IAA consisting of four biodiversity hotspots: the Indo-Burma, Philippines, Sundland and Wallacea (Myers *et al*. 2000), phylogenetic, phylogeographic and conservation biology studies have lagged behind other parts of the world (Sodhi and Liow 2000) leaving this incredible diversity is under threat from human activities (Lohman *et al*. 2011).

The aim of this study was to resolve the phylogeographic relationship of murid rodents from Tarutao National Park within the islands in the National Park and also with their mainland relatives using a multi-disciplinary approach (external and skull morphometrics and DNA sequences). We tested the hypothesis that the genetic differences if observed among the population should also be reflected in the morphology and metrics of the populations or groups.

To analyze the evolutionary relationships of murid rodents within the five islands in Tarutao National Park and also between mainland and island populations, two species were used as model species. The species that were selected are the ones which were present on most of the islands that are included in this study and also because these two species have two different biological behaviors with *R. tanezumi* being associated more with people (McNeely and Lekagul 1988, Corbet and Hill 1992, Chaimanee 1998, Francis 2008) and hence likely to reflect if there are any human-related reintroduction and/or gene flow between the mainland and the National Park while *M. surifer* is a strictly forest species and not associated with human habitats (Gorog *et al*. 2004) so it's likely to have established on the island when it was still connected to the mainland hence likely to reflect the past history of the distribution of the habitats between the mainland and these Islands.

The two species were also chosen because their taxonomy in the Tarutao National Park is not very well understood as the initial specimens of these species collected were assigned different names (as subspecies) from their mainland relatives based some differences which were observed by Miller (1900), and Chasen (1940), however both could not ascertain the taxonomic status of these species because they didn't have enough samples to do the comparisons and because they based their description on the morphology of a few museum specimens. However, these first descriptions have now been clumped as synonyms of *R. tanezumi* and *M. surifer* without reassessing the validity of those names. Therefore, motivated by this information, we conducted this study to collect fresh samples and compare as many specimens of these species as possible and also use both morphological and molecular data sets to reassess the phylogenetic relationships of these populations of murid rodents from this National Park in relation to their mainland relatives and within the islands in the National Park.

The findings of this study will be help in answering whether there are any significant differences between the populations of these murid rodents on the islands and also whether the current taxonomic status of the specimens from Tarutao National Park is valid or not. Because we also employ molecular data, it will also better the current knowledge of the historical biogeography of this National Park. Later the results from this study may also help to provide advice to the national park management on the need for conservation of these rodents and also which species or islands in the national park should be prioritized for conservation purposes if any interesting differences between the island and mainland populations were to be found. Finally we will discuss the adaptive nature of the patterns of variation in these murid rodents based on the three data sets employed in this study.

MATERIALS AND METHODS

a) Molecular Analyses

Extraction and Preservation of Tissue Sample for Molecular Analysis

For the specimens that were sacrificed for further studies of the skull and later preserved as voucher specimens, the liver and tongue was obtained from the specimen as soon as possible after sacrificing the animal and these tissues were immediately placed in separate tubes containing 95% alcohol. The tubes were tightly sealed and placed in ice while in the field and transferred to the refrigerator once back in the laboratory. For the specimens that we released while in the field, the tip of the tail was obtained for molecular analysis and in some cases a piece of the ear was also obtained from the animals if the tail was incomplete or in bad condition. These tissues were also stored in the same way as for the liver and tongue in tubes containing 95% alcohol. The field specimen labels were put on each tube containing the tissue for that particular specimen to avoid mismatching the tubes with tissues samples with the specimens from whom they were obtained (figure 18). Later the tissues were sent for processing at the Canadian Centre of DNA Barcoding in the United States of America. Two mitochondrial genes (cytochrome *b* (cyt-*b*) and cytochrome c oxidase I (COI)) and one nuclear gene were used to cross-match the identifications of species with its morphology, to determine how long the island population has been isolated from the mainland and see the phylogenetic relationship between Island and mainland populations and also within the Islands in the National Park.

Figure 18. Tools used in collecting and storing the tissue samples (liver and tongue).

DNA amplification and PCR protocols

The tissues samples were sent to the Canadian Center for DNA Barcoding (CCDB) and three genes (COI, Cyt b and IRBP) were sequenced following the following protocols.

For the COI gene, the standard methods for mammal barcoding were followed (Ivanova and Grainger 2007a, 2007b, Francis *et al*. 2010).

For both Cyt b and IRBP total genomic DNA was extracted following the semi-automated glass fiber DNA extraction protocol (Ivanova *et al*. 2006) with minor modifications. In brief, tissue was incubated overnight in 50 µl of Vertebrate Lysis Buffer with Proteinase K. A volume of 50 µl of lysate was transferred to a clean plate and used for semi-automated DNA extraction on the Biomek FX liquid handling station using Acroprep 96 well plates with 1 µm GF membrane (PALL Corporation). DNA was eluted in 80 µL of 10 mM Tris-HCL, pH 8.0. The DNA products were then read to run PCR.

For Cyt b in an attempt to recover full length of the gene, two PCR reactions were conducted using different sets of primers. In the first case, each PCR reaction contained a total volume of 12.5 µl consisting of 5% trehalose (D-(+)-Trehalose dehydrate), 1.25 µl of 10x reaction buffer (Life Technologies, Invitrogen), 2.5 mM of $MgCl_2$, 2.5pmol each of forward (CCHCCATAAATAGGNGAAGG (MTCB-F)), and reverse (WAGAAYTTCAGCTTTGGG (MTCB-R)) primers (Naidu *et al*. 2012), 50 μM of dNTP, 0.3 U of KAPAHotStart DNA Polymerase (KapaBiosystems Inc., Boston, USA), and 2 μl of DNA template. PCR cycling was then performed with an initial denaturation at 94C for 5 min, followed by 35 cycles of denaturation at 94 C for 45 sec, annealing at 55 C for 1 min, extension at 72 C for 2 min and a final extension step at 72 C for 10 min. PCR products were visualized on a 2% agarose gel E-gel® (Invitrogen) as described in (Ivanova and Grainger 2007a).

In the second case for Cyt b, each PCR reaction contained a total volume of 12.5 μl consisting of 5% trehalose (D-(+)-Trehalose dehydrate), 1.25 μl of 10x reaction buffer (Life Technologies, Invitrogen), 2.5 mM of $MgCl_2$, 1,25pmol each of forward (CCATCCAACATCTCAGCATGAT (CB1-5)) modified from Kocher *et al*. (1989) and reverse (GGCAAATAGGAARTATCATTC (CB3A)) (Kocher *et al*. 1989) primers, 50 μM of dNTP, 0.3 U of KAPA HotStart DNA Polymerase (KapaBiosystems Inc., Boston, USA), and 2 μl of DNA template. Here the thermo cycle consisted of 94°C for 1 min, five cycles of 94°C for 40 sec, 45°C for 40 sec, and 72°C for 1 min, followed by 35 cycles of 94°C for 40 sec, 51°C for 40 sec, and 72°C for 1 min, with a final extension at 72°C for 5 min (Hajibabaei *et al*. 2005, deWaard *et al*. 2008). PCR products were also visualized on a 2% agarose gel E-gel® (Invitrogen) as described in (Ivanova and Grainger 2007a).

For IRBP, only one PCR reaction was done. Each PCR reaction contained a total volume of 12.5 μl consisting of 5% trehalose (D-(+)-Trehalose dehydrate), 1.25 μl of 10x reaction buffer (Life Technologies, Invitrogen), 2.5 mM of $MgCl_2$, 2.5pmol each of forward (ATGGCCAAGGTCCTCTTGGATAACTACTGCTT (IRBP217)) and reverse (CGCAGGTCCATGATGAGGTGCTCCGTGTCCTG (IRBP1531)) primers (Stanhope *et al*. 1992), 50 μM of dNTP, 0.3 U of KAPAHotStart DNA Polymerase (KapaBiosystems Inc., Boston, USA), and 2 μl of DNA template. Then the PCR procedure was as follows: an initial denaturation of 5 min at 95°C, 2 cycles of 40 s at 94°C, 40 s at 65°C, 70 s at 72°C, and 34 cycles of 40 s at 94°C, 40 s at 58°C, 70 s at

72°C. The final extension lasted for 10 min at 72°C. Also the PCR products were visualized on a 2% agarose gel E-gel® (Invitrogen) as described in (Ivanova and Grainger 2007a).

Finally PCR products generated with IRBP217/IRBP1531 and MTCB-F/MTCB-R were purified with 0.5:1 beads to template ratio using AlinePCRclean kit (AlineBiosystems) to remove non-specific low molecular weight products; CB1-5-CB3A products were sequenced without purification. All PCR products were bidirectionally sequenced using corresponding sequencing primers as described in (Ivanova& Grainger 2007b) on 3730XL sequencer. CodonCode Aligner 4.1.1 (CodonCode Corporation) was used for sequence editing and assembly of bidirectional contigs.

Sequence and phylogenetic Analyses

The sequences for both species (*R. tanezumi* and *M. surifer*) were combined and analyzed together and two sequences of *Micromys minutes* (accession numbers BZ02 and BZ07) were downloaded from the NCBI database and used as out groups in all analyses.

The DNA sequences for each data set (Cyt, CO1 and IRBP) were aligned separately using Clustal W (incorporated in MEGA 5.2.1 software) using the following default DNA alignment parameters: gap opening penalty = 15; gap extension penalty = 6.66 for both pairwise and multiple alignments; DNA weight Matrix = IUB; transition weight = 0.5; use negative matrix = off; and delay divergence cutoff (%) = 30 (these parameters are given here for the sake of repeatability only) and were verified manually. In the final analyses, 1140 base pairs (*bp*) of cytochrome *b*, 657 bp of CO1 and 1186 bp of IRBP were used. All the sequences used in this study are given in appendix 7 (cytochrome *b* gene), appendix 8 (cytochrome oxidase 1 (CO1) gene), and appendix 9 (inter-retinoid binding protein (IRBP) gene).

24 maximum likelihood fits of different nucleotide substitution models were computed using MEGA version 5.2.1 software (Tamura *et al*. 2011) . The most appropriate model of gene evolution was determined from the 24 models by selecting the model with the lowest Bayesion Information Criterion (BIC) and Akaike Information Criterion corrected (AICc) values (Nei and Kumar 2000). The corresponding parameters for that model for each data set were used in the subsequent phylogenetic analyses. Phylogeny reconstruction and tree construction were performed for three statistical methods (maximum likelihood (ML), minimum evolution (ME), and neighbor joining (NJ) using MEGA 5.2.1 software on each data set. For each data set the mean distances (uncorrected '*p*' distances) were computed between groups (island groups and mainland) using MEGA version 5.2.1 (Tamura *et al*. 2011).

The divergence times were estimated from neighbor joining trees for mtDNA genes (cyt b and CO1) data sets using a "standard molecular clock of 2% Myr^{-1} for mammalian mtDNA (Brown *et al*. 1979), a rate that is consistent with that estimated from raw differences in *Rattus* and *Mus* cyt b sequence calibrated with fossil split of these two genera (Jacobs and Downs 1994).

Finally the haplotype diversity and network were calculated using DnaSP version 5.10 (Librado and Rozas 2009) and drawn in Network version 4.6.1.1 (www.fluxus-engineering.com) by using median joining method (Bandelt *et al*. 1999)

b) Morphological and Morphometric Analyses

Measurement and Description of External and Cranial Characters

External characters refers to such things as size, shape, length of legs, ears and tail, shape of nails, claws, size and shape of feet and footpads, number of mammae, and color of the specimen (McNeely and Lekagul 1988) while cranial characters are the measurements on the skull.

Firstly, the specimens captured in the field where identified based on morphological features following Francis (2008) and some were collected as voucher specimens and the skull was extracted and compared with other literature (Miller 1900, Chasen 1940, Hill 1960, McNeely and Lekagul 1988, Lunde and Son 2001). The age and sex of the specimens was determined following Aplin *et al.* (2003), Barnett and Dutton (1995), Cunningham and Moors (1996) and Francis (2008) (figures 19 and 20). All the specimens included in the analysis were considered to be adult individuals based on careful observation the morphological and pattern of tooth wears on the occlusal surface. The taxonomy in this study we followed (Musser and Carleton 2005). Additional specimens were accessed from the Princess Maha Chakri Sirindhorn Natural History Museum (Prince of Songkhla University, Thailand), Thailand Natural History Museum (Pathumthani Province, Thailand) and importantly specimens used by Miller (1900) were loaned from the United States National Museum (USA).

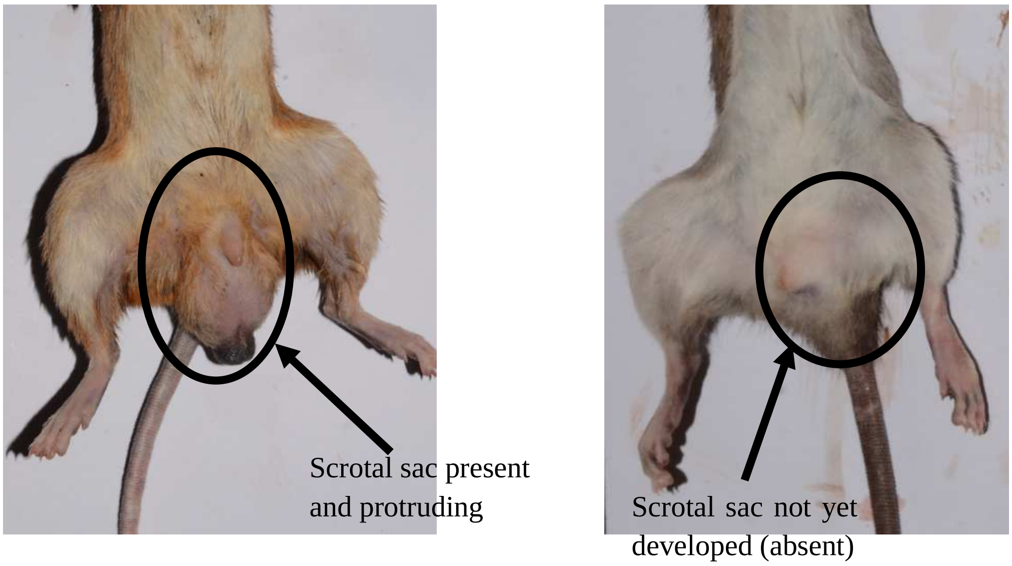

Figure 19. Comparison between adult (left) and immature/juvenile (right) male individuals.

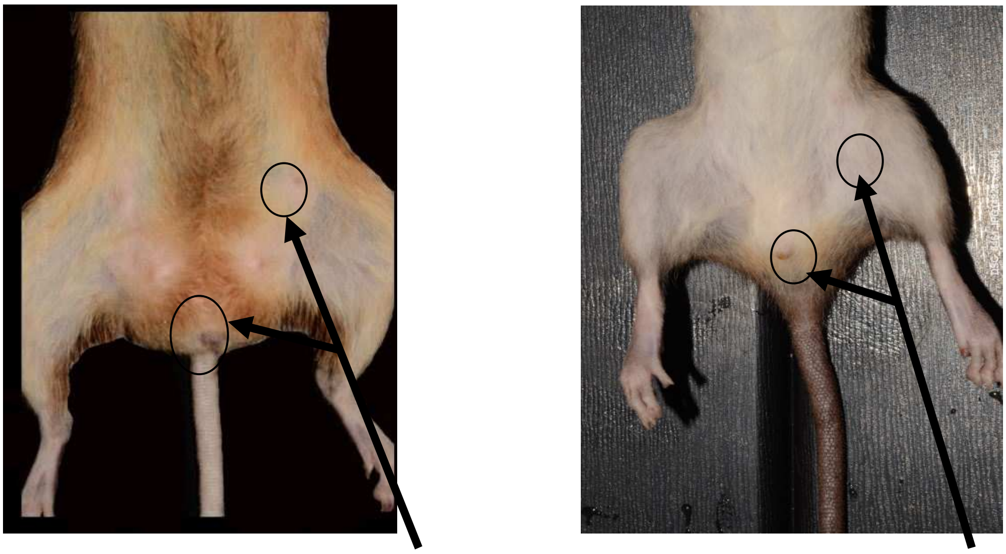

Figure 20. Comparison between adult (left) and juvenile (right) female individuals.

Then the following standard external measurements (figure 21) were taken with a digital caliper to the nearest 0.01mm for the specimens captured in the field while for museum specimens the measurements were recorded from the attached labels from the museum specimen.. These were; Tail length (**T**): measured from the anus to tip of fleshy or bony part of the tail excluding hairs that project beyond the tip; head and body length (**HB**): measured from the anus to the tip of nose when the animal is stretched out; hind foot length exclusive of claws (**HF**): measured from the heel to the tip of longest toe excluding the claw; and ear length (**E**): measured from the base of the external opening of the ear to the tip of the ear. The description of the external characters that were in this study followed Lunde and Son (2001) and Francis (2008). Additionally the body weight (**W**) of adult specimens was obtained by the use of a Pesola spring balance in grams (g).

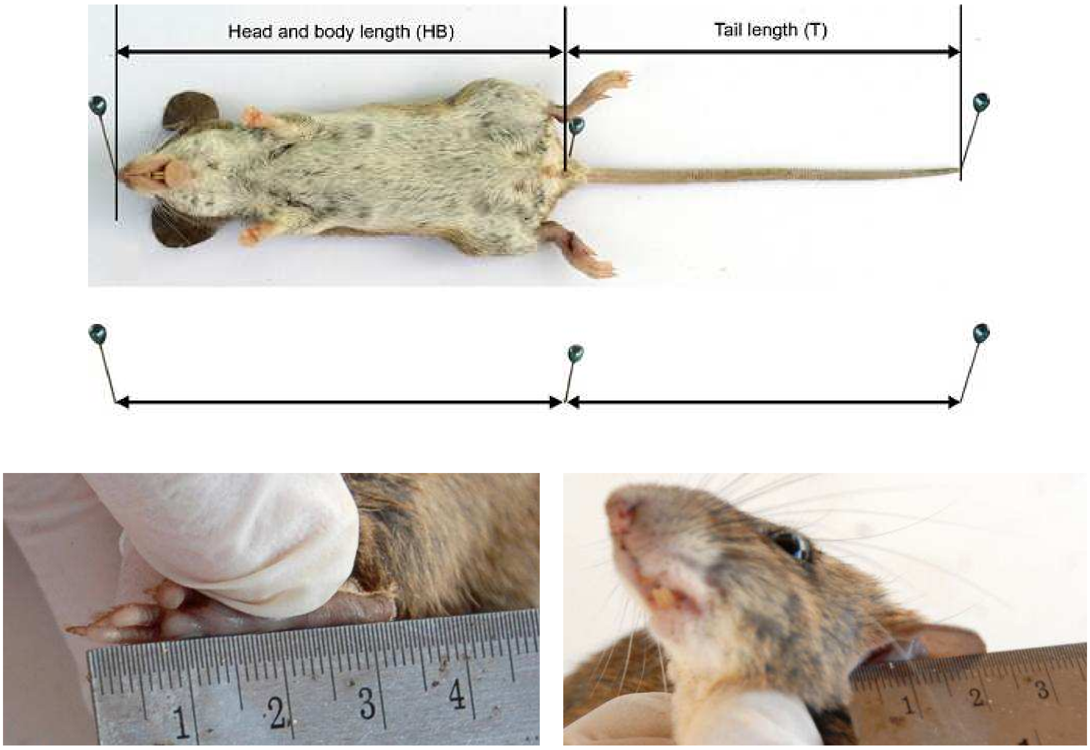

Figure 21. External measurements used; HB, T, HF and E respectively (Herbreteau *et al*. 2011).

Finally, the skulls of voucher specimens collected in the field were prepared following methods described by Sutherland (2000) with a few modification and then twenty one (23) cranial measurements (figure 23) were taken on all the specimens used for this study also using a digital caliper to the nearest 0.01mm by one person to reduce interpersonal error in measurements: (1) **Greatest Length of Skull (GSL)**: the longest distance from the tip of the rostrum to the posterior most part of the skull; (2) **Breadth of Braincase (BBC)**: the greatest width of the braincase posterior to the zygomatic arches. This is measured from just above the squamosal root of each zygomatic arch; (3) **Height of Braincase (HBC)**: the greatest height of the skull from the top of the braincase to the ventral surface of the basisphenoid bone; (4) **Breadth of Rostrum (BR)**: the greatest breadth across the rostrum, including the bony capsules enclosing the nasolacrimal canals; (5) **Length of Rostrum (LR)**: the distance from the tip of the nasal bones to the posterior margin of the zygomatic notch (the anterior edge of the dorsal maxillary root of the zygomatic plate); (6)

Interorbital Breadth (IB): the narrowest breadth between the orbits, and anterior to the posterior processes when present; (7) **Zygomatic Breadth (ZB)**: the greatest breadth/width across the zygomatic arches; (8) **Breadth of Zygomatic plate (BZP)**: the least distance between the anterior and posterior edges of the zygomatic plate; (9) **Length of Diastema (LD)**: the distance from the posterior alveolar margins of the upper incisors to the anterior alveolar margins of the first upper molars; (10) **Post Palatal Length (PPL)**: the distance from the posterior margin of the palatal bridge to the posterior edge of the basioccipital bone – the ventral lip of the foramen magnum; (11) **Length of Bony Palate (LBP)**: the distance from the posterior edge of the incisive foramina to the posterior margin of the bony palate; (12) **Length of Incisive Foramina (LIF)**: the distance from the anterior edge of one of the foramina to its posterior edge; (13) **Breadth across Incisive Foramina (BIF)**: the greatest distance across both foramina; (14) **Length of Bullae (LB)**: the length of the auditory bullae, excluding the bony Eustachian tube; (15) **Length of Molar Tooth row (LM^{1-3})**: the distance from the anterior crown of the first molar to the posterior crown on the third molar; (16) **Breadth of First Molar (BM^1)**: the greatest distance from the labial crown to the lingual crown of the first molar; (17) **Breadth Across First Molars (BAM)**: the least distance between the lingual edge of the alveolus of the first molar and the lingual edge of the opposite molar; (18) **Breadth of Mesopterygoid Fossa (BMF)**: the distance from one edge of the mesopterygoid fossa to the other; (19) **Height of the mandible HM**; (20) **Length of mandible (LM)**; (21) **Length of lower Molar Tooth row (LM_{1-3})**; (22) **Length of Nasals (LN)**; and (23) **Palatal Length (PL)**.

All the cranial characters measured and the descriptions followed Carleton and Straeten (1997), Elbroch (2006), Francis (2008), Lunde and Son (2001), Musser and Durden (2002), Musser and Newcomb (1983), Musser *et al.* (2005). Musser *et al.* (2006), Nicolas *et al.* (2008b), Yoshida (1983), and Lin and Shiraishi (1992).

(a) (b) (c)

Figure 22. Photographs of field and laboratory research work; (a) specimen captured in the live trapping cage, (b) recording specimen data in the field with the help of my field assistants and (c) taking skull measurements in the laboratory.

Data Analysis

Statistical analyses on morphometric characters were performed using SPSS 16, R version 2.15.2 (R core Team, 2012), and PCORD version 5. Descriptive statistics for all the variables were computed using SPSS 16. We performed analyses of variance (ANOVA) using the GLM procedures in R program to assess the variations of morphometric variables on different islands and the mainland samples selecting $p<0.01$ and this helped us to group the specimens. We used $p<0.01$ as the limit of significance to exclude the possibility of sampling and/or measuring bias from affecting the results (Motokawa *et al*. 2003).

To assess the geographical variations, principle component analysis (PCA) based on correlation matrix for the different groups of specimens from the islands and mainland. Only cranial variables that were found to be significantly different groups from the ANOVA above were used for PCA because external were measured by different people and there could be inter person error in the measurements while all cranial variables were measured by one person.

When choosing the statistical tests, a key provided by Dytham (2011) for choosing a statistical test and also the literature from other studies of this nature were extensively utilized. It is also important to note that prior to any statistical analysis, all data were assessed for normality and homogeneity of variance.

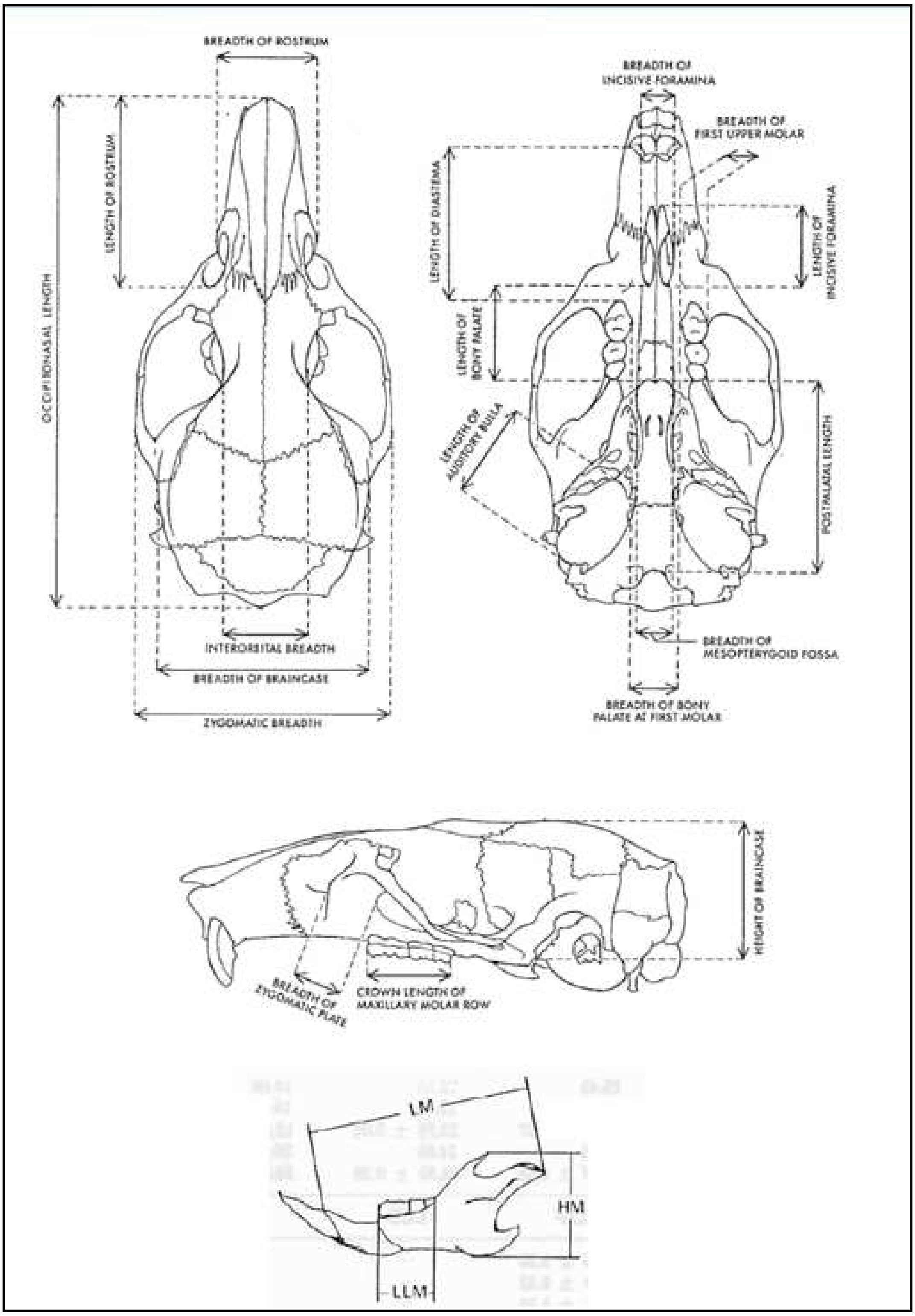

Figure 23. Schematic representation of the skull showing the cranial characters measured (Lin and Shiraishi 1992, Musser et al. 2006). See text above for explanation of the characters and abbreviations.

RESULTS

a) Phylogenetic Analyses

Cytochrome *b* data set;

The topology of the boostrap consensus tree (figure 24) from maximum likelihood analyses explained the cyt b data set much better than the neighbor-joining and minimum evolution trees and hence this was chosen to present the result of the cyt b data set. Three distinct clades (numbered 1, 2, and 3 on figure 24) were obtained for *R. tanezumi*. Clade 1 consisted of the specimens from Taruato and Yang Islands and a single specimen from the mainland (Songkhla). Clade 2 constituted the two other specimens from the mainland (Trang and Chumphon) clustered together with specimens from Rawi and Butong Islands. The specimens from Adang island and a single individual clustered together to form clade 3. The uncorrected '*p*' distances varied from 0.00 (0%) to 0.07 (7%) between the groups (table 4). A molecular clock performed using neighbor-joining showed that clade 2 diverged first approximately 1.7 Mya from clades 1 and 3. The divergence between Clades 1 and 3 was estimated to have taken place about 1.2 Mya. The haplotype diversity, Hd, in *R. tanezumi* was calculated to be 0.7879 and 9 different haplotyes were recovered (figure 25)

Table 4. *R. tanezumi* estimates of evolutionary divergence (uncorrected '*p*' distance values) over sequence pairs between groups for cyt *b* gene using TN93+G model in MEGA v5. Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated leaving a total of 715 positions in the final dataset, 'n' is the sample size.

	n	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1. Tarutao	14		0.010	0.001	0.001	0.008	0.010	0.010	0.008	0.010
2. Trang	1	0.055		0.010	0.010	0.011	0.004	0.004	0.010	0.003
3. Songkhla	1	0.003	0.056		0.000	0.009	0.010	0.010	0.008	0.010
4. Yang	3	0.003	0.056	**0.000**		0.009	0.010	0.010	0.008	0.010
5. Adang	5	0.047	**0.070**	0.048	0.048		0.011	0.011	0.006	0.011
6. Rawi	5	0.054	0.010	0.054	0.054	**0.070**		0.000	0.010	0.003
7. Butong	2	0.054	0.010	0.054	0.054	**0.070**	**0.000**		0.010	0.003
8.Tarutao (08)	1	0.044	0.063	0.045	0.045	0.026	0.060	0.060		0.010
9. Chumphon	1	0.057	0.007	0.058	0.058	0.068	0.006	0.006	0.061	

For *M. surifer* also three distinct clades (labeled A, B, and C on figure 24) were obtained. Clade A had specimens from the mainland (Songkhla), clade B contained specimens from Adang and Rawi Islands, and clade C had all the specimens from Tarutao Island. The uncorrected '*p*' distances varied from 0.007 (0.7%) to 0.042 (4.2%) between the groups (table 5). A molecular clock performed using neighbor-joining showed that clade A separated from clades B and C approximately 1.0 Mya and the divergence between clades B and C was placed at about 500, 000 years ago. The haplotype diversity, Hd in *R. tanezumi* was calculated to be 0.7 and 7 different haplotyes were recovered using median joining (figure 26).

Table 5. *M. surifer* estimates of evolutionary divergence (uncorrected '*p*' distance values) over sequence pairs between groups for cyt *b* gene using TN93+G model in MEGA v5. Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated leaving a total of 714 positions in the final dataset, 'n' is the sample size.

	n	**1**	**2**	**3**	**4**
1. Songkhla	4		0.008	0.008	0.008
2. Rawi	2	**0.042**		0.003	0.006
3. Adang	5	0.041	**0.007**		0.005
4. Tarutao	14	0.039	0.020	0.019	

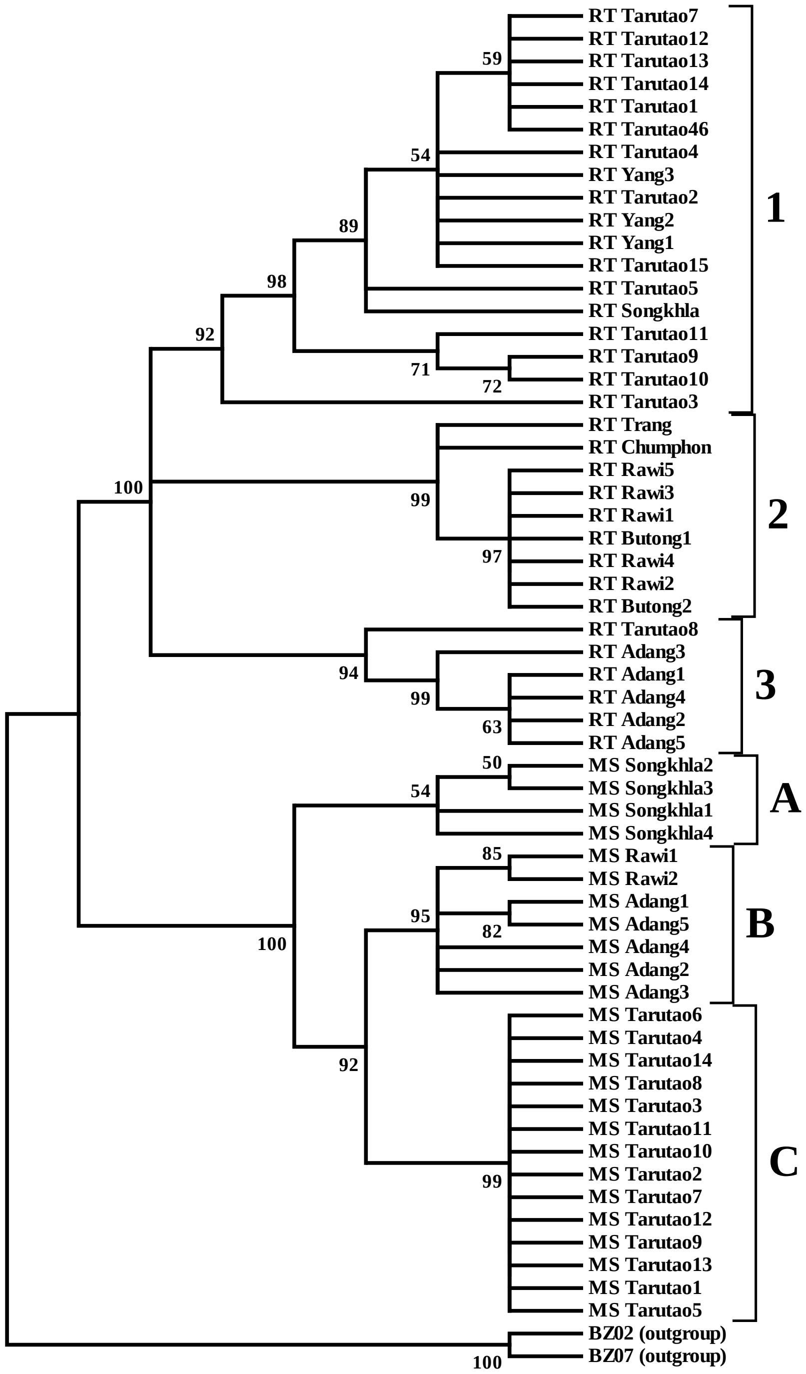

Figure 24. Bootstrap consensus tree for the cytochrome *b* data set, phylogenetic reconstruction using Maximum Likelihood based on Tamura-Nei model for both *R. tanezumi* (RT) and *M. Surifer* (MS). The numbers next to the branches represent the percentage of replicates trees in which the associated individuals clustered together in the bootstrap test (1000 replications). The out group used was *Micromys minutes* (BZ02 and BZ07 represent the accession numbers in the gene bank)

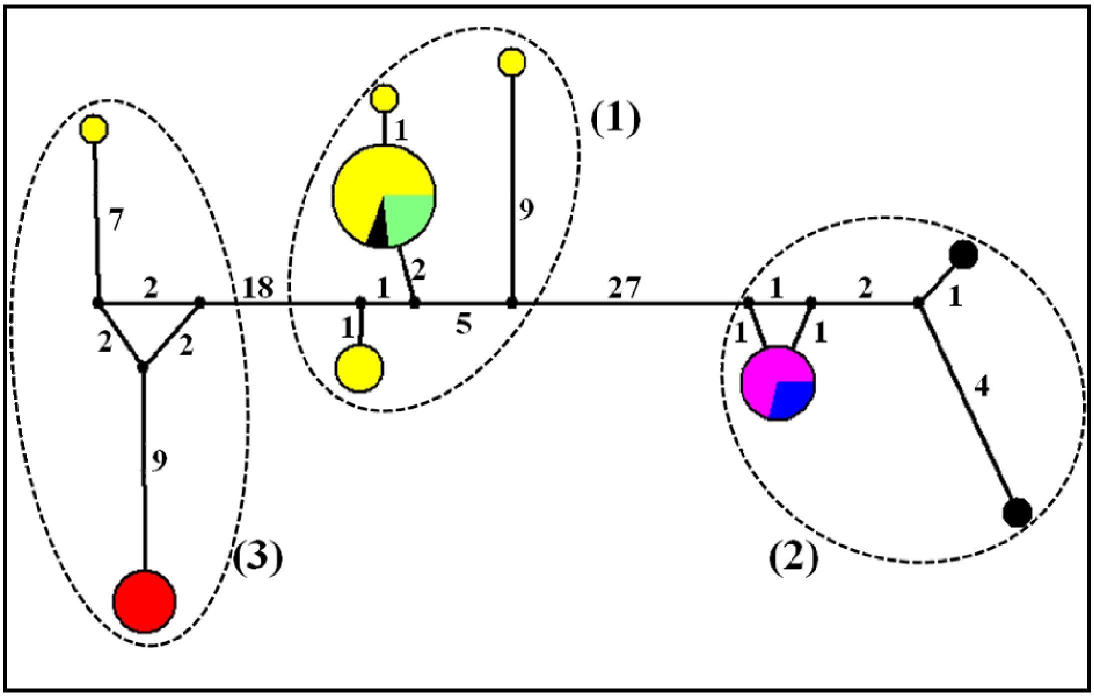

Figure 25. Haplotype network of *R. tanezumi* cyt b data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow; Adang Island specimens = red; Rawi Island specimens = purple; Butong Island specimens = blue; Yang Island specimens = green; and Mainland specimens = black). The numbers in brackets corresponds to the numbering of clades in figure 24.

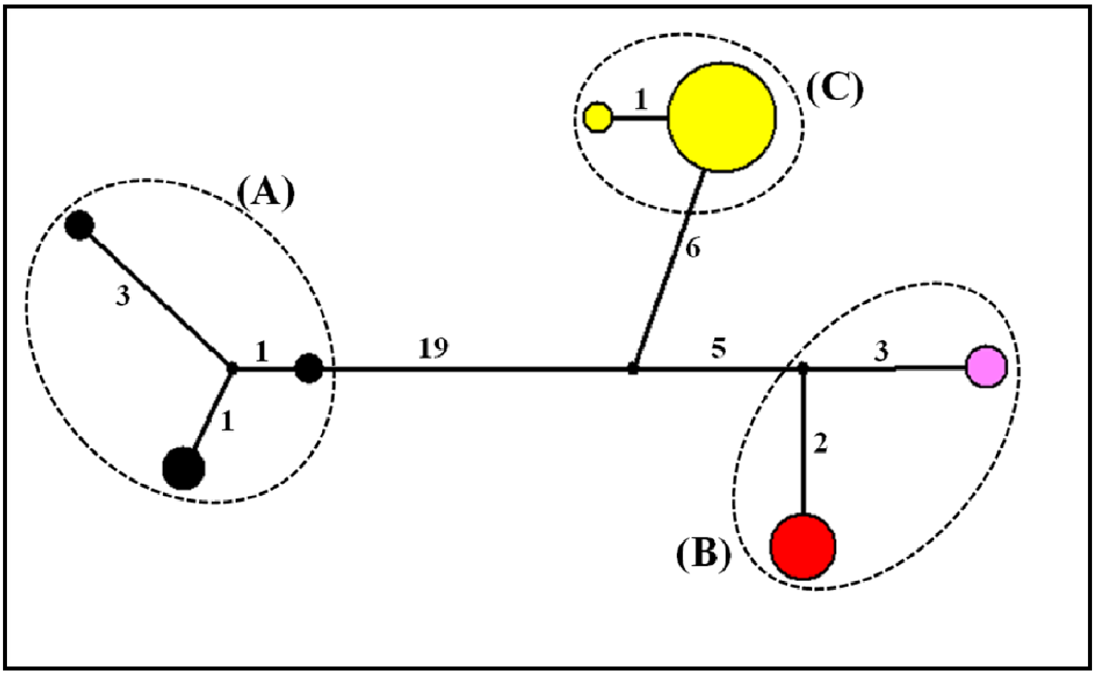

Figure 26. Haplotype network of *M. surifer* cyt b data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow; Adang Island specimens = red; Rawi Island specimens = purple; and Mainland specimens = black). The letters in brackets corresponds to the letters of clades in figure 24.

COI data set;

Maximum likelihood bootstrap consensus tree (figure 27) gave a better topology than the neighbor-joining and minimum evolution trees. Again three clades were recovered for both *R. tanezumi* and *M. surifer* and the composition of the clades was not different to that observed from cyt *b* data set even though the resolution of the clades was better in the cyt *b*.

For *R. tanezumi*, the uncorrected *'p'* distances between the clades ranged from 0.000 (0%) to 0.066 (6.6%) (table 6). The divergence times were estimated to have taken place around 1.8 Mya between clade 3 and the other two clades, while clades 1 and 2 separated approximately 1.0 Mya. The haplotype (gene) diversity (Hd) was 0.803 (SD= 0.054) and the data set contained 11 unique haplotypes (figure 28).

Table 6. *R. tanezumi* estimates of evolutionary divergence (uncorrected '*p*' distance values) over sequence pairs between groups for COI gene using Tamura-Nei model in MEGA v5. Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated leaving a total of 650 positions in the final dataset, 'n' is the sample size.

	n	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1. Tarutao	14		0.010	0.001	0.001	0.008	0.010	0.010	0.008	0.011
2. Trang	1	0.063		0.010	0.010	0.011	0.003	0.003	0.010	0.004
3. Songkhla	1	0.002	0.062		0.000	0.008	0.010	0.010	0.008	0.011
4. Yang	3	0.002	0.062	**0.000**		0.008	0.010	0.010	0.008	0.011
5. Adang	5	0.038	**0.066**	0.037	0.037		0.010	0.010	0.005	0.011
6. Rawi	5	0.061	0.005	0.060	0.060	**0.063**		0.000	0.010	0.003
7. Butong	2	0.061	0.005	0.060	0.060	**0.064**	**0.000**		0.010	0.003
8. Tarutao (08)	1	0.040	0.060	0.039	0.039	0.017	0.058	0.058		0.010
9. Chumphon	1	0.066	0.066	0.066	0.066	0.066	0.008	0.008	0.060	

On the other hand, the uncorrected '*p*' distances between the clades for *M. surifer* varied from 0.00 (0%) to 0.019 (1.9%) (table 7). A molecular clock performed using neighbor-joining showed that clade A diverged first approximately 400,000 ya from clades B and C. The divergence between Clades B and C was estimated to have taken place about 200,000 ya. The haplotype diversity, Hd, in *M.surifer* was calculated to be 0.7708 and 8 different haplotyes were recovered (figure 29)

Table 7. *M. surifer* estimates of evolutionary divergence (uncorrected ‘*p*’ distance values) over sequence pairs between groups for COI gene using TN93+G model in MEGA v5. Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated leaving a total of 626 positions in the final dataset, ‘n’ is the sample size.

	n	**1**	**2**	**3**	**4**
1. Songkhla	4		0.005	0.005	0.005
2. Rawi	2	**0.019**		0.000	0.003
3. Adang	5	**0.019**	**0.000**		0.003
4. Tarutao	14	0.014	0.005	0.005	

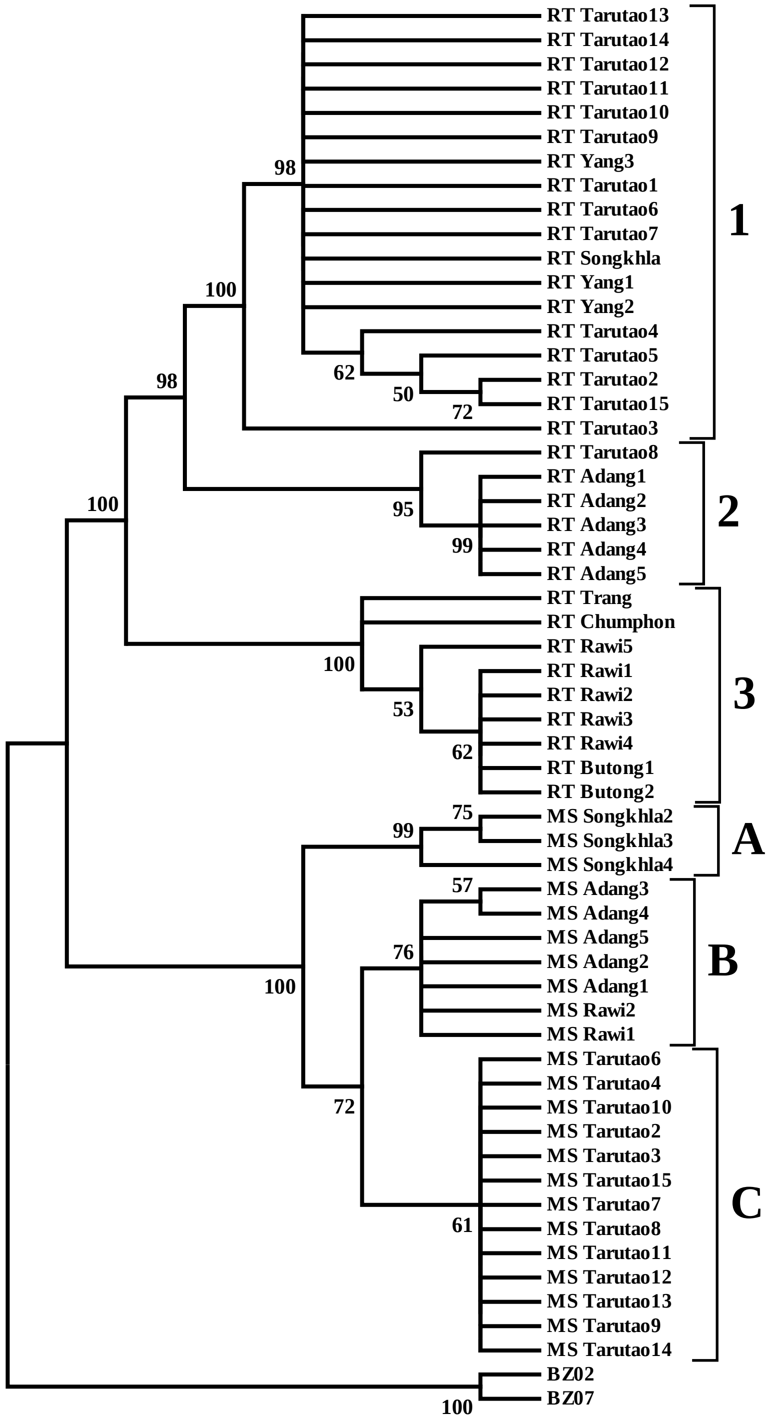

Figure 27. Bootstrap consensus tree for the cytochrome oxidase 1 (CO1 gene) data set, phylogenetic reconstruction using Maximum Likelihood based on Tamura-Nei model for both *R. tanezumi* (RT) and *M. Surifer* (MS). The numbers next to the branches represent the percentage of replicates trees in which the associated individuals clustered together in the bootstrap test (1000 replications).

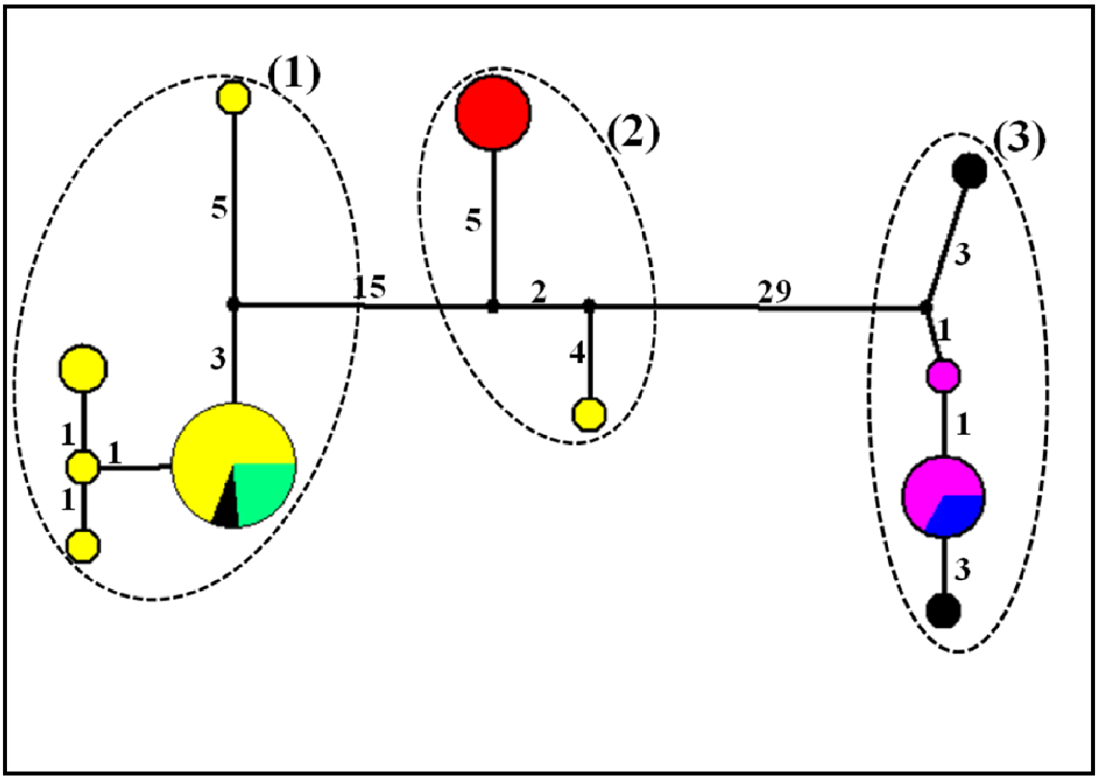

Figure 28. Haplotype network of *R. tanezumi* COI data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow; Adang Island specimens = red; Rawi Island specimens = purple; Butong Island specimens = blue; Yang Island specimens = green; and Mainland specimens = black). The numbers in brackets corresponds to the numbering of clades in figure 27.

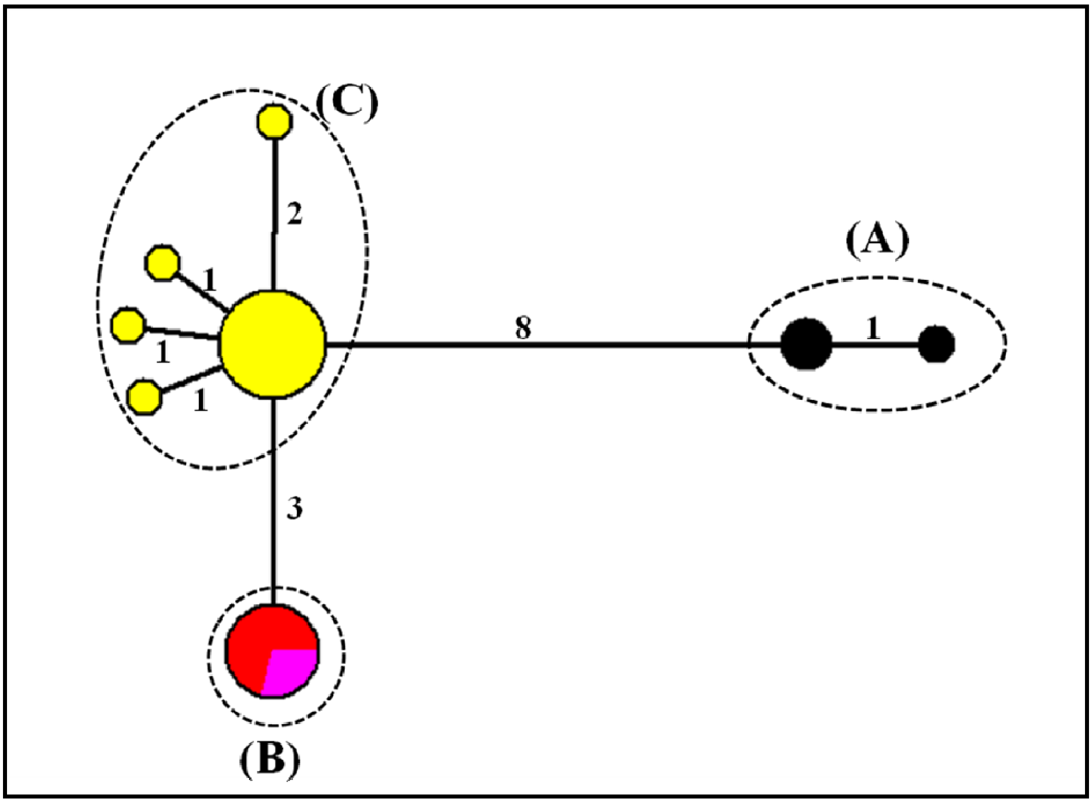

Figure 29. Haplotype network of *M. surifer* COI data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow; Adang Island specimens = red; Rawi Island specimens = purple; and Mainland specimens = black). The letters in brackets corresponds to the letters of clades in figure 27.

IRBP data set;

Maximum likelihood bootstrap consensus tree (figure 30) gave a better topology than the neighbor-joining and minimum evolution trees. From figure 30, two main clades were recovered for *R. tanezumi*, clades 1 and 2. Clade 1 containing all specimens from Tarutao Island, interestingly within the Tarutao clade, a sub clade 1.1 was also recovered and this was also confirmed when minimum evolution tree (figure 31) used analyzed. Unfortunately for *M. surifer* only specimens from Tarutao Island were sequenced and all the individuals clustered together in clade C (figure 30). However, on analysis of minimum evolution, a sub clade (C.1) was resolved (figure 31).

The haplotype diversity, Hd, in *R. tanezumi* was calculated to be 0.8363 and 6 different haplotyes were recovered (figure 32). For *M. surifer*, even though all the specimens were from the same Tarutao Island, the haplotype diversity was calculated to be 0.6818 and 6 distinct haplotypes were recovered (figure 33)

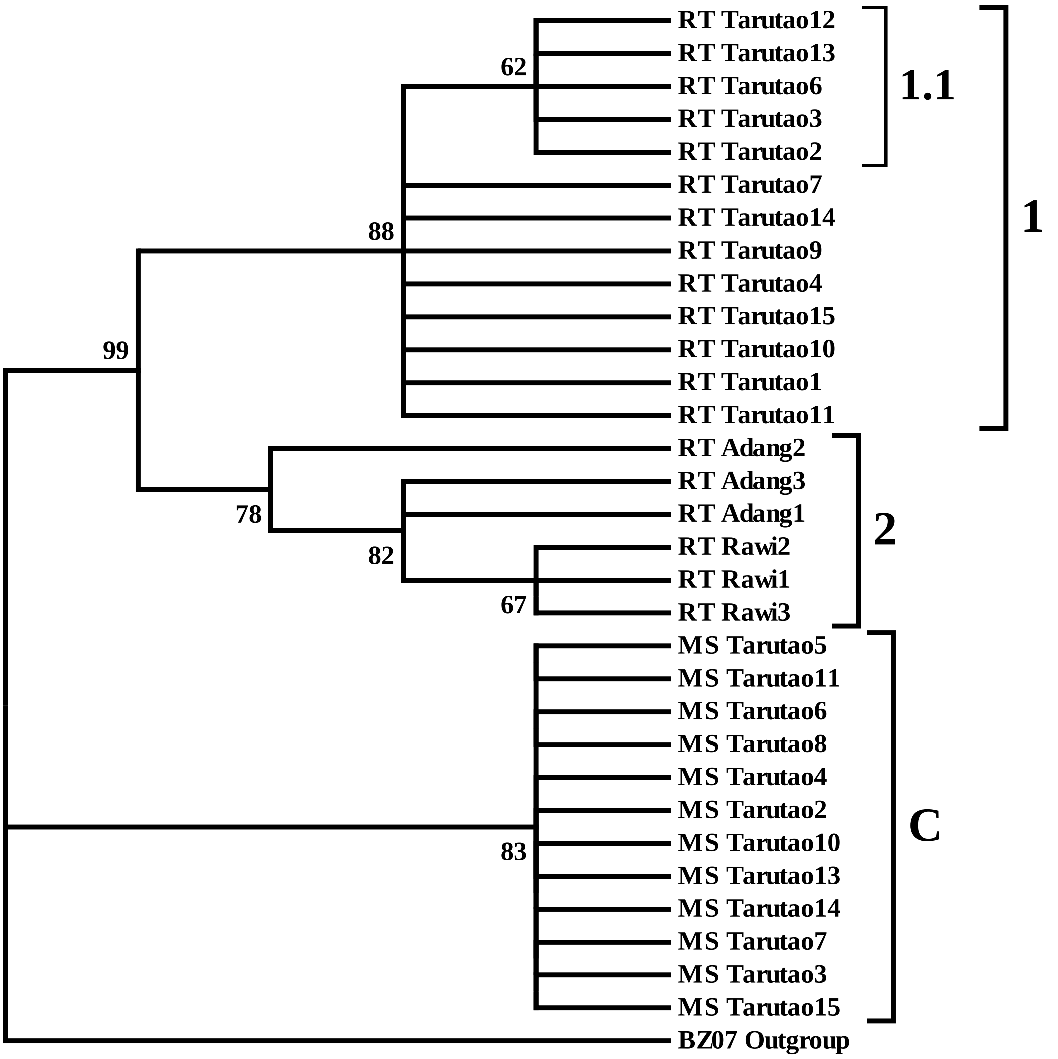

Figure 30. Bootstrap consensus tree for the IRBP data set, phylogenetic reconstruction using Maximum Likelihood based on Tamura-3-parameter model for both *R. tanezumi* (RT) and *M. Surifer* (MS). The numbers next to the branches represent the percentage of replicates trees in which the associated individuals clustered together in the bootstrap test (1000 replications).

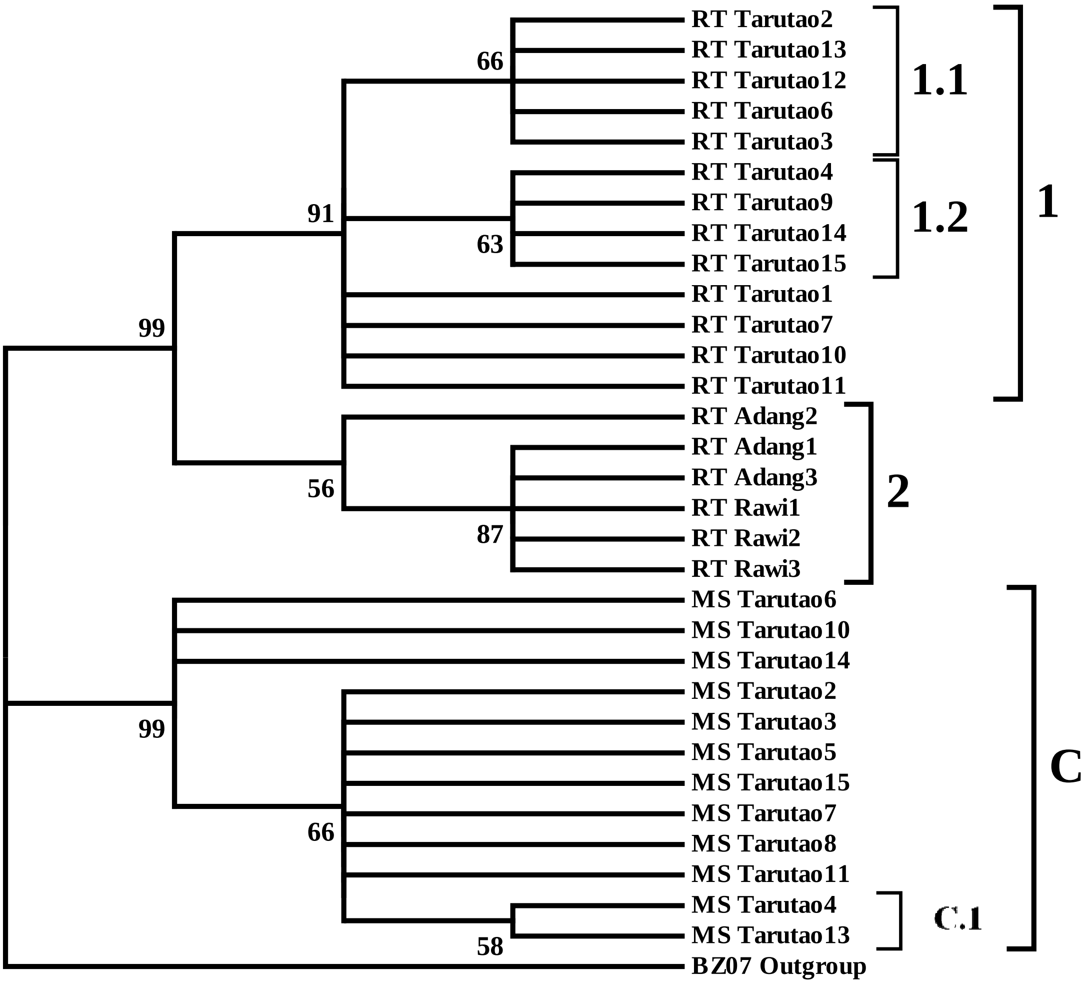

Figure 31. Bootstrap consensus tree for the IRBP data set, phylogenetic reconstruction using minimum evolution based on Tamura-3-parameter model for both *R. tanezumi* (RT) and *M. Surifer* (MS). The numbers next to the branches represent the percentage of replicates trees in which the associated individuals clustered together in the bootstrap test (1000 replications).

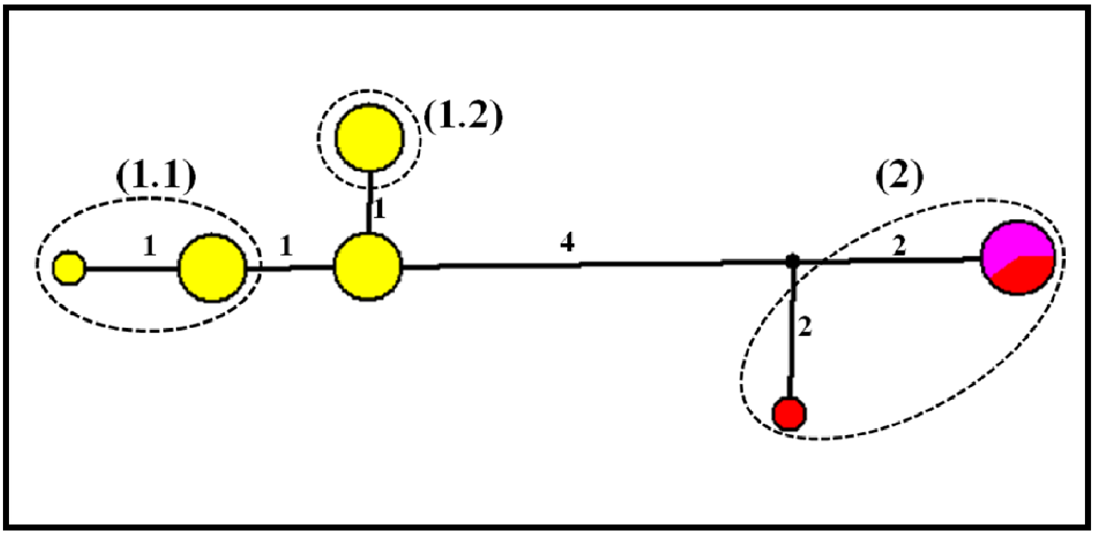

Figure 32. Haplotype network of *R. tanezumi* IRBP data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow; Adang Island specimens = red; and Rawi Island specimens = purple). The numbers in brackets corresponds to the numbering of clades in figures 30 and 31.

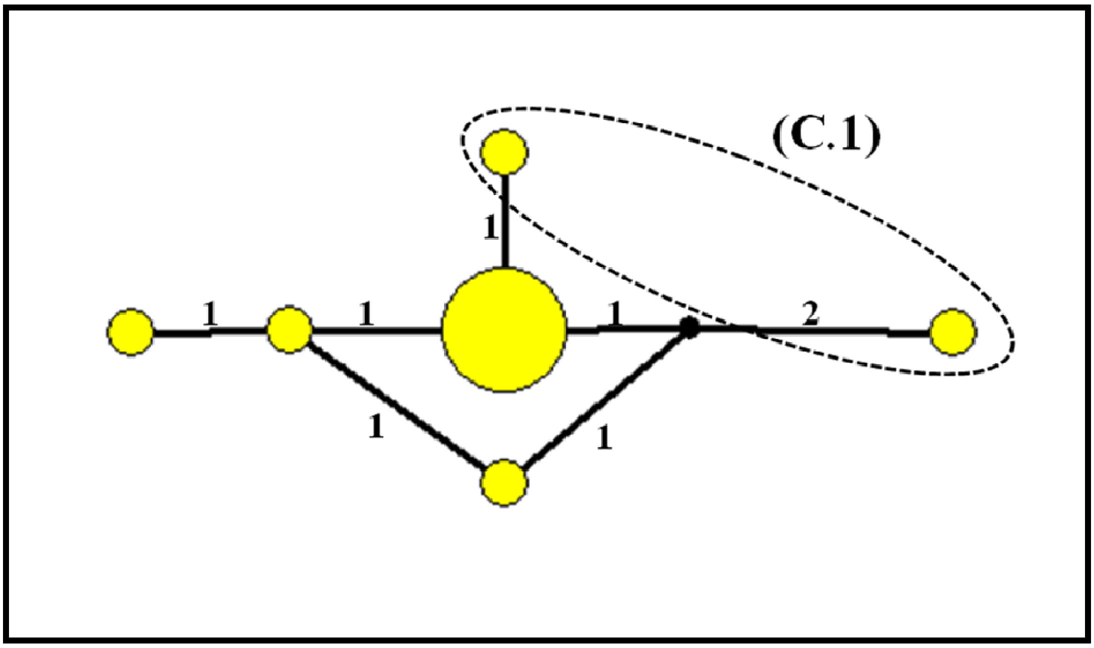

Figure 33. Haplotype network of *M. surifer* COI data set using median joining method. Each circle represents a specific haplotype. Branches represent mutational steps between haplotypes and the numbers on the branches show the exact number of mutational steps. The size of the circle corresponds to the number of individuals with that particular haplotype. (The colors represent; Tarutao Island specimens = yellow). The letters in brackets corresponds to the letters of clades in figure 30 and 31.

b) Morphological Analyses of External and Skull Variations.

The coloration of the mainland and island forms in *M. surifer* is not very different even though the island forms tend to have darker dorsum with less dispersed black guard hairs while in the mainland forms the dorsum is brighter with more guard hairs tending to concentrate on the middle. Ventrally, the island samples had a belly somewhat ochraceoues orange, a few having creamy white color which was characteristic of the mainland specimens. However, in both island and mainland forms the separation between the ventrum and dorsum can be easily seen on the sides. The specimens from the Islands had distinctively shorter tails than head and body length while in mainland specimens, the tail length and head and body length were almost equal.

In the skulls of *M. surifer* it was found that the specimens the all islands had the similar shape which showing some differences with the mainland specimens (figure 34). Firstly it was found that all specimens of *M. surifer* from the Islands were deep ridged in outline on the braincase than were specimens from the mainland. Another difference that can be easily noticed between the Islands and mainland specimens is the shape of the Interpariental. The specimens from the Islands had a more triangular interparietal than the specimens from the mainland (figure 31). Other skull features looked the same in shape differing only in measurement (Appendix 1) with the island specimens having larger values than Mainland specimens.

The coloration of both mainland and all islands forms of *R. tanezumi* was not different. The only difference was that the specimens from Tarutao and Yang islands had soft fur and lacked guard hairs while the specimens from Adang, Rawi, and Butong islands had stiff guard hairs given then a spinous dorsum. All the external measurements (Appendix 3) were not significantly different although with Tarutao Island specimens having a mixture of large and small size individuals while Rawi, Adang and Butong tended to skew towards large body size and mainland and Yang island samples skewing towards smaller size. All in all it is very difficult to separate the specimens from these localities based on the.

Suffice to say also that the shape of the skull of individuals from both the mainland and islands observed showed no differences in morphology (figure 35). However, the mainland and Yang island specimens had only smaller size skulls, Tarutao island specimens having a mixture of large and small size skulls while Rawi, Adang and Butong had distinctively larger skulls only. But no differences in shape could be observed.

Figure 34. Representative skulls of *Maxomys surifer*. Left skull representative of mainland specimens and right the skull representative of island specimens (scale bar 5mm).

Figure 35. Representative skulls of *R. tanezumi*. Left skull representative of mainland specimens, in the middle skull representative of Tarutao and Yang islands specimens and finally on the right the skull representative of Adang, Rawi and Butong islands specimens (scale bar = 5mm).

c) Multivariate Analyses of Cranial Variations

The sample size, means, SD, minimum and maximum values of adult specimens only which were used in statistical analyses from all the localities are summarized in Appendix 1 for *M. surifer* and Appendix 3 for *R.tanezumi*.

From one-way analysis of variance (1-way ANOVA) of samples from these islands and the mainland sample in *M. surifer,* it was found that there was no significant difference in all the morphometric (both external and cranial) variables measured between Adang and Rawi islands at $p<0.01$. Therefore, in the later analyses the samples from these two islands was pooled together as one sample considering also the fact that the sample size from Rawi island was very small ($n= 2$). Two (Tail and HF) external and Fourteen (GSL, LR, IB, BBC, IFM^1, LBP, PPL, BMF, BAM, BIF, LM^{1-3}, BM^1, LM, and LM_{1-3}) cranial variables were found to be significantly different ($p<0.01$) from the ANOVA results. A posthoc scheffe's test was then conducted to see which variables had statistically significant different means between the groups of samples and it was found that the means of BBC, IFM^1, BMF, and LM were not significantly different at $p<0.01$ level in all the groups hence these variables were not included the later multivariate (PCA) analyses. The F statistic, p value, r^2 and adjusted r^2 and posthoc scheffe's results of all external and cranial variables used in this study are summarized in Appendix 2.

From the PCA results it was found that Adang and Rawi specimens grouped together than mainland specimens while Tarutao island specimens had a mixture of both large skulls overlapping with Adang and Rawi island specimens and small skulls overlapping with mainland specimens (figures 36 & 37).

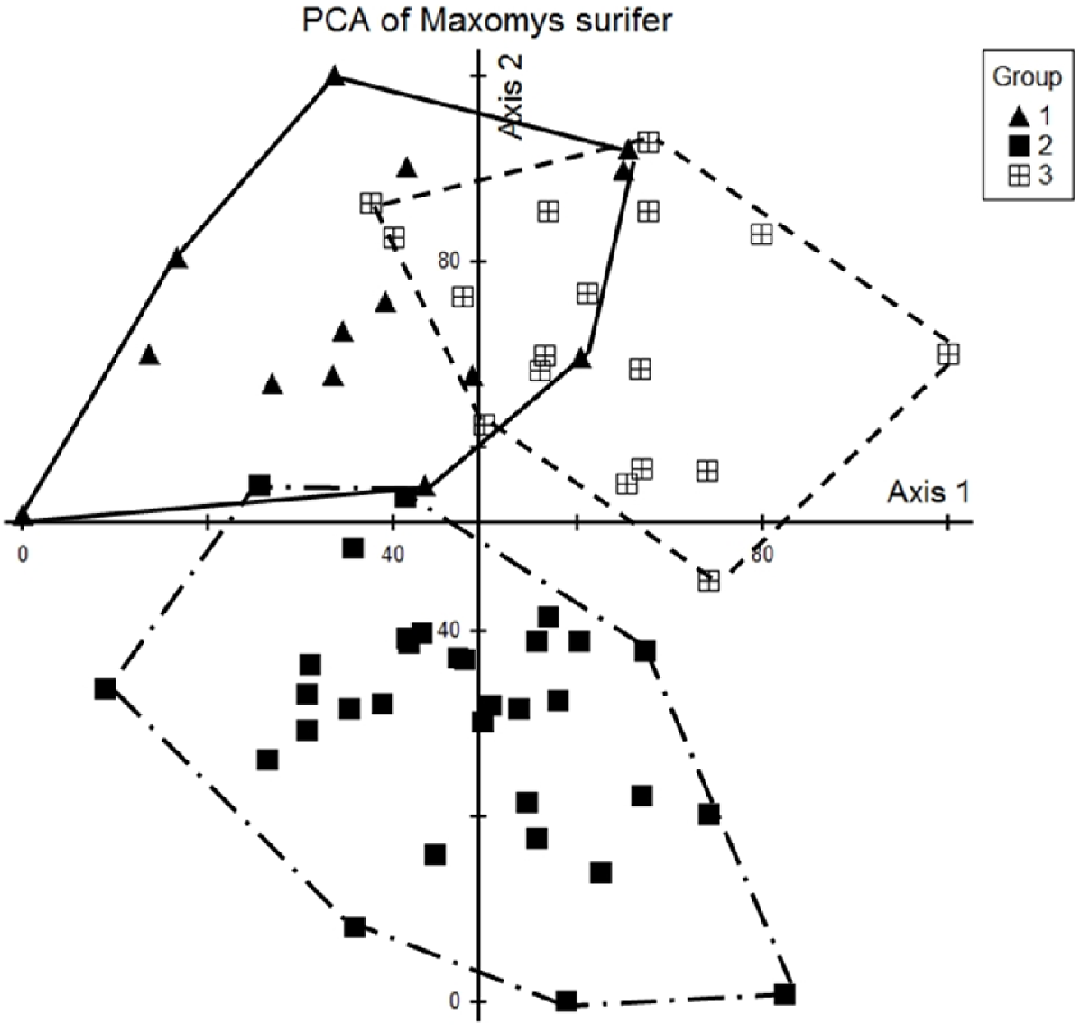

Figure 36. Principle component analysis (PC1 vs PC2) based 10 cranial variables (Appendix 5) from three clades of *Maxomys surifer* defined by molecular analyses of cyt *b* and COI. Closed triangles (1) = specimens from Adang and Rawi islands (clade B); Closed squares (2) = specimens from Tarutao Island (clade C); and Crosses in squares (3) = specimens from mainland (clade A). See Appendix 5 for variance explained the contribution of the variables on each axis.

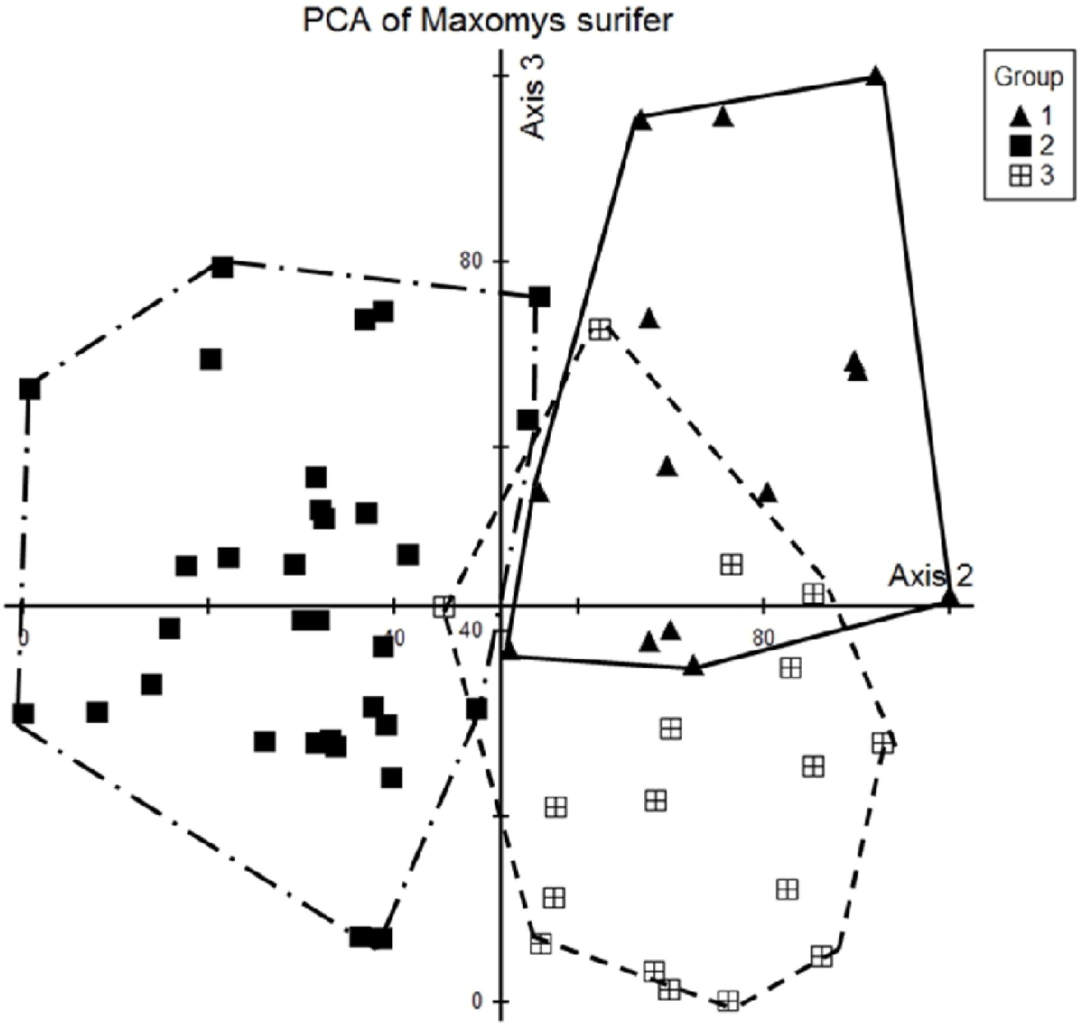

Figure 37. Principle component analysis (PC2 vs PC3) based 10 cranial variables (Appendix 5) from three clades of *Maxomys surifer* defined by molecular analyses of cyt *b* and COI. Closed triangles (1) = specimens from Adang and Rawi islands (clade B); Closed squares (2) = specimens from Tarutao Island (clade C); and Crosses in squares (3) = specimens from mainland (clade A). See Appendix 5 for variance explained and the contribution of the variables on each axis**.**

For *R, tanezumi*, the 1-way ANOVA results after a posthoc scheffe's test showed that the specimens from Adang, Rawi and Butong were not different in terms of morphometircs and these were pooled together in PCA analyses, but there were significantly different from Tarutao, Yang and Mainland samples (Appendix 4). After a posthoc scheffe's test was conducted to see which variables had statistically significant different means between the groups of samples, 8 skull variables (appendix 6) were found to be significantly different among at least two groups and these were later used to run PCA in PC-ORD 5. The *F* statistic, *p* value, r^2 and adjusted r^2 and posthoc scheffe's results of all external and cranial variables used in this study are summarized in Appendix 4.

From the PCA plots, it was found that specimens from Adang, Rawi and Butong grouped together and separated from the specimens from Yang, Tarutao and mainland which also formed another group that could not be separated (figure 38 and 39).

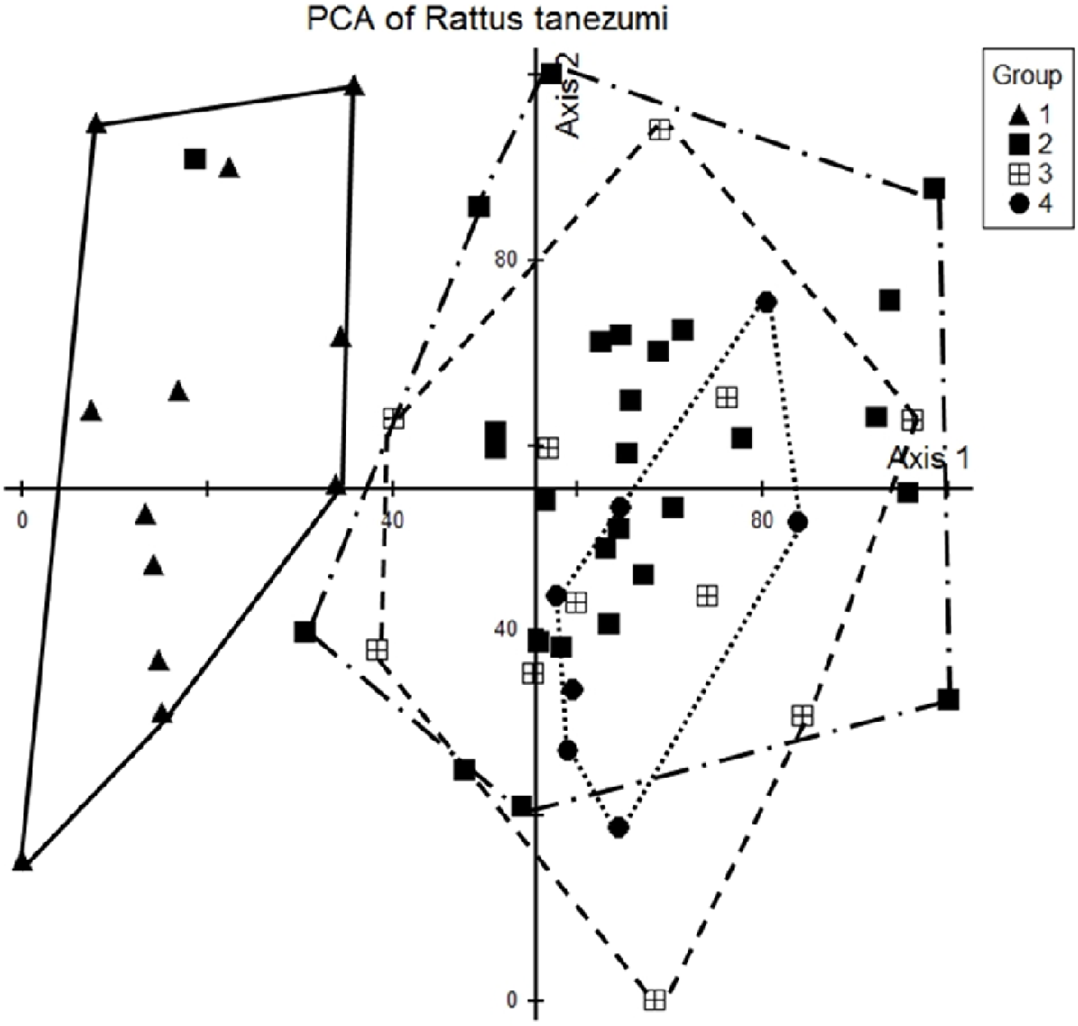

Figure 38. Principle component analysis (PC1 vs PC2) based 8 cranial variables (Appendix 6) from three clades of *Rattus tanezumi* defined by molecular analyses of cyt *b* and COI. Closed triangles (1) = specimens from Adang and Rawi islands (clade B); Closed squares and filled circles (2, 4) = specimens from Tarutao and Yang Islands (clade C); and Crosses in squares (3) = specimens from mainland (clade A). See Appendix 6 for variance explained and the contribution of the variables on each axis

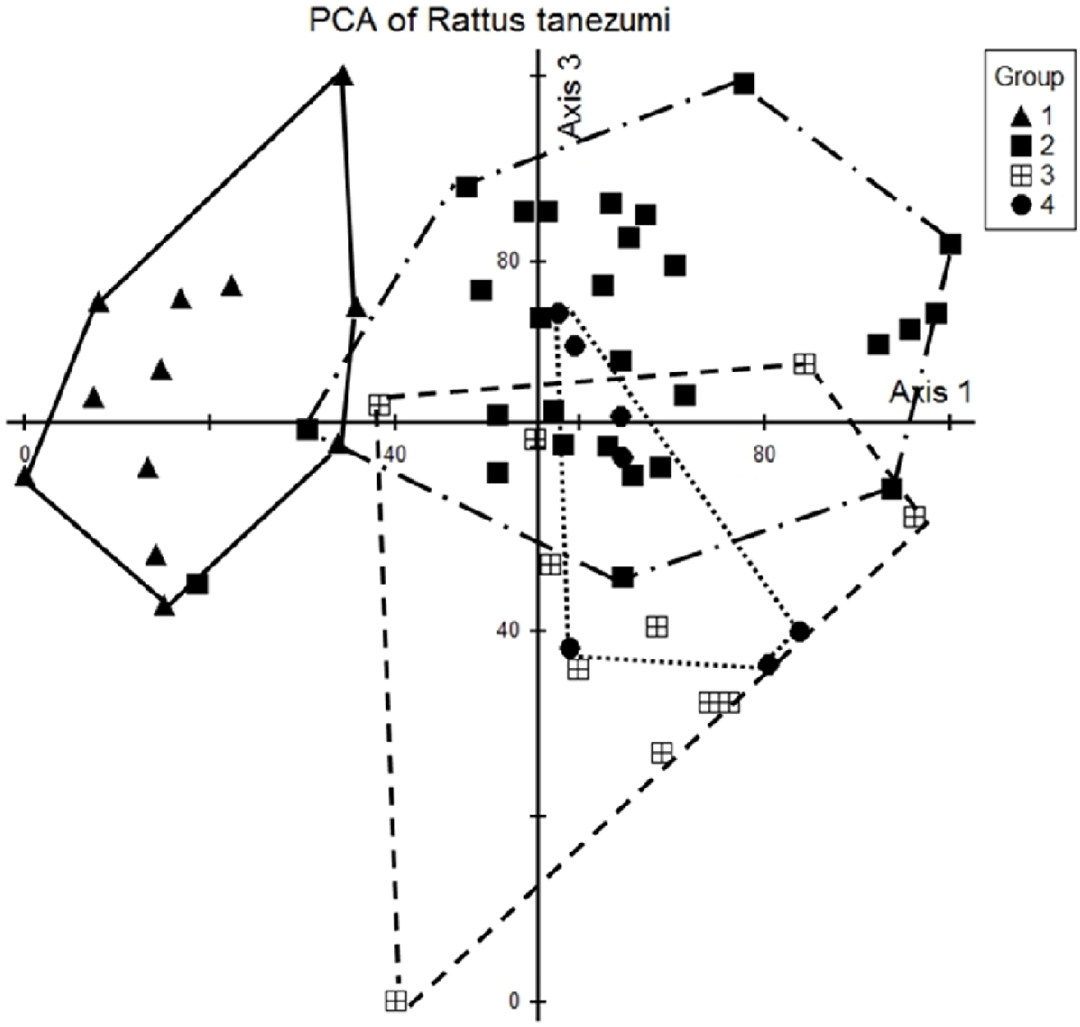

Figure 39. Principle component analysis (PC1 vs PC3) based 8 cranial variables (Appendix 6) from three clades of *Rattus tanezumi* defined by molecular analyses of cyt *b* and COI. Closed triangles (1) = specimens from Adang and Rawi islands (clade B); Closed squares and filled circles (2, 4) = specimens from Tarutao and Yang Islands (clade C); and Crosses in squares (3) = specimens from mainland (clade A). See Appendix 6 for variance explained and the contribution of the variables on each axis**.**

DISCUSSION

This study aimed at elucidating the phylogenetic relationship of murid rodents within five islands in Tarutao National Park and also with their closest mainland relatives using a multidisciplinary approach. Two species (i.e. *R. tanezumi* and *M. surifer*) were used as model species for this study. Using these various data sets, the two species not only revealed striking differences in their patterns of relationships among the populations but also the overlooked first description of these species from Tarutao National Park especially in the case of *M. surifer*. The molecular result of *M. surifer* recovered monophyletic clades in all the two mitochondrial genes which show biogeographic patterns of variation in genetics and morphology but this clear separation could not be recovered in *R. tanezumi* (figures 24 and 27).

Our molecular results for *Maxomys surifer* support the ideas by Miller (1900) who called the specimens from the islands from Adang and Rawi islands as *M. surifer butangensis* and Chasen (1940) who called the specimens from Tarutao Island as *M. surifer flavidulus* both based on the morphological differences they observed (also confirmed in this study) between the populations of *M. surifer* from Tarutao National Park and their mainland relatives. Therefore, the question that remains critical here is whether those subspecies names should be brought recognized again or these populations should continue be called *Maxomys surifer* when they are clearly genetically and morphologically isolated (but maybe not reproductively isolated) from the true *Maxomys surifer* series from the mainland? Though this might be debatable, based on the results from this study, I would reconsider raising the populations of *Maxomys surifer* series from Tarutao National Park to be subspecies of the mainland forms based on the evidence of our study.

The difference in the pattern showed between the two species used in our present study reflect the importance of understanding the biology of the species to choose as a model when attempting to reconstruct the historical biogeography of the area or region. This is because species such as tree shrews which have the ability to colonize a wide range of habitats may not reveal a great deal of information of the past distribution of habitats either through their present distribution pattern or genetic make-up (Ruedi 1996) and this was the case for *R. tanezumi* which is a commensal species introduced to most islands by humans (McNeely and Lekagul 1988, Corbet and Hill 1992, Meijaard 2003, Francis 2008). While a species which is more forest-dependent (*M. surifer*) is more likely to show the past history of the habitats either through their present distribution, morphology or genetics (Gorog *et al.* 2004). This was also raised by Lohman *et al.* (2011) that phylogeographic require analysis of rapidly evolving markers and dense sampling of rainforest-dependent taxa to understand the past habitat of Sunda Shelf during the Pleistocene period. The results showed that a forest dependent species is more suitable to infer historical biogeography of archipelagos than commensal species because of the possibility of reintroduction hence continued gene flow between the populations or groups.

Although our aim was not to estimate the exact divergence dates, the recovery of three sister monophyletic clades in the forest-depedent – *M. surifer* – with no shared haplotypes among the lineages gives an impression of a deep vicariance process baring in mind that the islands in Tarutao National Park are estimated to have separated from the mainland Thailand about 9500 years ago. Therefore, it is reasonable to assume that even though these islands where connected to the mainland during the Last Glacial Maximum (LGM), the populations of murid rodents on these islands were separated before this time and also that the areas connecting these islands to the mainland could have been not suitable for these populations to mix and hence still acted as a barrier. This explanation can be supported from the evidence that Palaeoenvironments of insular Southeast Asia during the LGM were more cooler and drier thus inhospitable for rain forest species (Gorog *et al*. 2004, Bird *et al*. 2005, Lohman *et al*. 2011).

From the mitochondrial DNA results, it was found that even though the topology of the trees was not different, the haplotype networks were different and it was found that cyt b showed a higher resolution of the differences between the populations than COI especially between Adang and Rawi samples. Whereas COI should that the specimens from these islands had the same haplotypes, cyt b was able to separate them into having different haplotypes. This is probably because cyt b is a much longer gene (1200 bp) compared to COI (657 bp) and it can be concluded that the longer the gene the more information it would provide and the better the resolution of the relationships between the populations. Therefore, it can be said that haplotype networks seemed to give a clear pattern of groupings than phylogenetic trees which just show grouping and common ancestry but cannot show the origin of the groupings very well and cannot also show how many mutational steps are their between the difference groups or clades.

Despite the data for the nuclear IRBP gene not being sufficient (i.e. we could not sequence from all the islands and mainland), it showed the potential of being able to resolve the phylogenetic relationships of the specimens with the topology similar to that in both mtDNA. Another interesting result from this data set was that for both species within the Tarutao Island there seems to be one main population and another a subpopulation. Because Tarutao Island is large, this might represent a step in sympatric evolution within the population on this Island in both species which after a long time would lead to formation of two separate genetically distinct populations. Therefore, it would be interesting if we could have the sequences from all the individuals for both mtDNA and nuclear IRBP and combine the data sets to see how the tree would look like, however, this was a limitation for us and we had to run each gene separately.

Our results of both the external and cranial measurements taken were increasing the further you move from the mainland in both species (with the exception of specimens from Yang Island). This was also true in terms of the coloration with mainland forms being brighter in *M. surifer* and moving towards more dark away from the mainland while in *R. tanezumi* the mainland forms had soft guard hairs and moving away from the mainland the hardness of the guard hairs increased. Therefore, I would strongly here to assume that this is probably represents a step in evolution with the Tarutao Island specimens having a mixture of old and new characters while Rawi, Adang and Butong specimens have lost most of the similarity with the mainland forms as also proposed though on a lighter note by Hill (1960) because he didn't have enough samples from the islands.

The smaller tails of insular *M. surifer* from Tarutao National Park as comapared to their mainland relatives may give us an insight that the temperatures in this National Park have been hotter than on the mainland. According to Burnstock *et al*. (2006), the artery inside the rat tail is very important for balance and thermoregulation with up to 20% of the total body heat loss of the rat accounted for by the tail. This is because of the rat tail hairless thus providing a large surface area to volume ratio for heat loss and in addition it is highly vascularised with arteriovenous anastosomes (Gordon 1990), hence the short tails in the islands samples can be explained as a way adapting to the cold temperatures on the islands especially at night when the individuals are active searching for food (Francis 2008). Thus the short tails would be a morphological advantage to them for conserving heat and also help when escaping from predators or competitors (such as tree shrews which compete for the same food resource with them) on these islands.

This difference were the island forms in both species being larger in terms of the skull size can be explained in terms of the island rule which states that smaller vertebrates on mainland tend to be larger on islands and the opposite is the case for larger vertebrates on mainland becoming smaller on islands. However, what is interesting is that according to the island rule that shape of the organism remains the same but only the size will increase or reduce the case observed in the skulls of *R. tanezumi*, on the other hand, this was not the case for *M. surifer* as the difference was not just in the size but also the shape as noted already above. This means that for *M. surifer* the island rule alone cannot explain the observed trend but there should be also some factors that are causing the island forms to change their shape of skulls. Similar results have been reported for small mammals in Southeast Asia (Heaney 1978) when he studied the tri-colored squirrel and this is believed to be a way to adapt to particular insular conditions (Lomolino 1985a, 2005). However, this trend (the island rule) seems to come from many factors such as population densities, immigration rates, food availability, introduction of predators, and environmental factors among others may lead to changes in size of insular populations in comparison to their mainland relatives. Amore comprehensive explanation on the island rule can be found in (Lomolino *et al*. 2006a)

In summary, it was found there is a distinct genetic isolation between island and mainland populations in *M. surifer* but this was not observed for *R. tanezumi* which we attributed to the earlier being a forest dependent and the later more commensal hence we feel that *R. tanezumi* would not be suitable in reconstructing the past history around this area as there could be some reintroductions from the mainland to the islands and also between the islands aided by humans movements and hence continued gene flow. Because of this genetic distinctiveness of *M. surifer* we would recommend that more phylogenetic studies should be conducted on a wider range of islands in Southeast Asia because almost all the specimens collected o the islands in this area were first assigned to subspecies level but now all clumped together as synonyms of *M. surifer* without any detailed assessment which would lead to underestimating how many species of *M. surifer* are actually in this region.

CHAPTER 5

GENERAL DISCUSSION AND CONCLUSIONS

This study is the most extensive study to be conducted in Tarutao National Park on murid rodents evident from both the number of Islands surveyed and also the numbers of individuals captured during the field work, it therefore, expand the current knowledge of murid rodents in known from three to five islands. Despite increase in the individuals recorded, the species list does not change very much. The current study also found the same species that were recorded on the Islands more than 100 years ago. This to some extent is an indication that the habitat on the Islands in Tarutao National Park has been undisturbed and hence the Islands are still supporting the same species over this period. However, with the increase in the numbers of Tourists in recent years visiting the National Park, the habitat is more likely to be disturbed in the quest to build more accommodation for the visiting tourists and this may have an effect on the species composition in the future.

In this study both based on the morphological and molecular data we didn't record *R. tiomanicus* which puts a question mark on its presence in the National Park, hence reducing the number of species to 4. It's highly possible that the specimens from Tarutao Island which were identified as *R. tiomanicus* were misidentified because of the highly similarity between the *R. tiomanicus* and *R. tanezumi* (Francis, 2008) or that the presence of *R. tanezumi* could have lead to the extinction or reduced population of *R. tiomanicus* as these are not usually found together on Islands (Cobet and Hill, 1992).

From the study of the biogeography on the murid rodents in this National Park it was found that Island area had a greater correlation with the species richness (r^2 = 0.882) than did the relative isolation (r^2 = 0.474) of the Islands from the mainland. However, it was realized that the lower r^2 value does not truly reflect the effect of Island isolation on the species richness in this National Park but this was because except for Tarutao Island, the other four islands had almost the same relative distance from the mainland. The distribution of the species in Tarutao Island were found to show a perfectly nested pattern were the species on the less rich islands were subsets of the more species rich Island. The idea of species-area relationship and species-isolation are very important to take into consideration especially in Southeast Asia where the habitat fragmentation is considered to be at highest in the tropics (Koh and Sodhi 2010) which leaves both vertebrates and plants threatened. Therefore, a clear understanding of these relationships can help in the conservation of the taxa in the fragmented habitats. The small area effect also helps us to be able to realize how big much of the forest we should protect in order to save the taxa in these fragments. A good example of the effect of habitat fragmentation (particularly on Islands) on the loss/extinction of small mammals can by drawn from within Thailand in a study by Gibson *et al*. (2013) where they “observed the near-total loss of native small mammals within 5 years from <10-hectare (ha) fragments and within 25 years from 10- to 56-ha fragments.” Therefore since Islands are of limited area, fragmentation would cause the biota on the Islands to undergo unprecedented anthropogenic threat coupled with natural, geography-induced population bottle neck (Lohman *et al*. 2011).

From our results on the phylogeography of murid rodents in Tarutao National Park, one important point that we found was that the use of a rainforest-dependent species (i.e *M. surifer*) showed a deep vicariance among the populations and the divergence times were more than in the commensal rat (i.e *R. tanezumi*). This result supports the suggestion by Lohman *et al*. (2011) that phylogeographic works in Southeast Asia will require dense sampling of rainforest-dependent taxa throughout Borneo, Java, Sumatra, and Thai-Malay Peninsula to determine whether a savannah corridor was a pervasive barrier to dispersal during the Pleistocene.” This result also corroborate that by Gorog *et al.* (2004) who also found a deep vicariant event in all three rainforest-dependent species of Murine rodents they used in their study. The commensal rat showed more of dispersal explanation leading to the sharing of haplotypes among the populations even though the divergence took place a long time ago, hence use of such a species to reconstruct the history would lead us to misinterpret the past.

Though not very significant, it is worth noting here that more studies of close populations should use longer genes if the genes being used are not rapidly evolving markers. This is because from the analysis of the haplotypes using cyt *b* showed that even close populations from Adang and Rawi islands had unique haplotypes but the shorter gene (COI) showed that the specimens from these two islands had the same haplotypes the difference most likely coming from the length of the genes. It can also be mentioned here that the nuclear IRBP gene seemed to give a deep resolution of the results, probably because the nuclear gene is inherited from both parents and hence showing a more clearer picture than the mitochondrial genes which are inherited from the mother only.

In summary, from the use of a multi-disciplinary approach, it was found the specimens of *M. surifer* from Tarutao National Park are genetically and morphologically distinct from their mainland relatives despite giving low uncorrected '*p*' distances. It was also evident that within Tarutao National Park, the specimens from Tarutao Island are genetically distinct from the specimens from Adang and Rawi Island. All this evidence points to the idea that the separation of these populations one the Islands have been separated for a long before the current approximation of when the Tarutao National Park Islands separated from the mainland. From these results it would be recommended that a further study of *M. surifer* should be conducted on the large scale by accessing the specimens from the Islands from around Southeast Asia and their mainland relatives. This is because what we are actually be calling *M. surifer* with a widespread distribution on both mainland and the Islands of Southeast Asia might actually represent a combination of different morphologically similar but genetically distinct population hence conservation measures should be applied differently especially for Islands populations which might be supporting small but distinct populations of *M. surifer* but may be suffering from high rates of extinction and endangerment just like most insular rodents (Amori *et al*. 2008). This might also be underestimating the actual number of species within what I will refer to as '*M.*

surifer group’ and such a study would also help to reconstruct the historical biogeography of Southeast Asia.

One the other hand, despite *R*, *tanezumi* high uncorrected ‘*p*’ distances values and a long divergence times than *M. surifer*, the specimens from the Islands and Mainland were found not to be genetically distinct from each other and was also evident in the sharing of the haplotypes among the specimens from different localities. Therefore, it is plausible to conclude that despite these populations having been separated a long time ago, there still is some genetic connectivity among the Islands and mainland specimens and this also explains why the specimens from Yang Island which in practical terms were expected to be genetically and morphologically similar to Adang, Rawi and Butong Islands because of its proximity to these Islands was found to be grouped together on all data sets with the Tarutao Island specimens and hence we can only assume that this is a new population that has just been introduced on the Island from Tarutao Island population.

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APPENDIXES

Appendix 1. Descriptive statistics of all external and cranial measurements of *M. surifer*. Adang (A), Rawi (R), Tarutao (T), and Mainland (M). Sample size is given in brackets (x). See text for the definition of the variables.

Variable		mean	SD	Min.	Max	Variable		mean	SD	Min.	Max.
W	A	173.00 (16)	25.73	135	230	**LR**	A	15.48 (12)	1.26	13.78	18.08
	R	180.00 (3)	10.00	170	190		R	15.55 (2)	0.37	15.28	15.81
	T	145.10 (29)	36.75	72	275		T	15.80 (34)	0.90	13.26	17.81
	M	136.25 (4)	37.72	100	180		M	14.72 (20)	0.78	13.14	16.31
HB	A	176.51 (16)	13.28	155.77	202.60	**BR**	A	7.78 (13)	0.48	7.00	8.50
	R	180.68 (3)	2.86	177.52	183.10		R	7.28 (2)	0.65	6.82	7.74
	T	176.83 (36)	11.00	142.00	200.00		T	7.92 (34)	0.39	7.16	8.92
	M	176.09 (16)	8.91	160.00	195.00		M	7.74 (20)	0.47	6.63	8.48
T	A	151.46 (16)	12.58	120.11	178.75	**LN**	A	17.32 (12)	1.09	15.44	18.84
	R	160.86 (3)	6.68	155.55	168.36		R	17.22 (2)	0.42	16.92	17.51
	T	169.00 (34)	8.78	149.80	190.10		T	17.64 (34)	0.91	16.05	19.49
	M	179.17 (16)	7.96	165.00	192.00		M	16.81 (20)	1.07	14.23	19.30
E	A	24.52 (16)	1.96	20.72	27.63	**IB**	A	7.70 (13)	0.32	7.34	8.33
	R	24.85 (3)	0.19	24.63	25.00		R	7.34 (2)	0.04	7.31	7.36
	T	24.42 (36)	1.94	19.80	27.40		T	7.24 (34)	0.32	6.44	7.80
	M	24.51 (16)	4.22	21.00	39.00		M	7.14 (20)	0.47	6.52	8.32
HF	A	37.72 (16)	1.67	34.56	40.73	**BBC**	A	16.73 (13)	0.50	15.48	17.43
	R	37.52 (3)	0.79	37.05	38.43		R	16.57 (2)	0.31	16.42	16.86
	T	38.74 (36)	1.94	32.10	42.20		T	16.49 (34)	0.39	15.49	17.21
	M	35.00 (16)	4.00	24.00	40.00		M	16.86 (20)	0.35	16.33	17.55
GSL	A	45.81 (12)	1.87	43.19	49.16	**ZB**	A	20.32 (11)	1.06	18.40	22.08
	R	46.34 (2)	0.08	46.28	46.39		R	20.85 (2)	0.76	20.13	21.21
	T	44.55 (34)	1.68	39.68	48.31		T	20.12 (34)	0.85	17.64	21.83
	M	43.66 (19)	1.41	39.82	46.02		M	19.75 (16)	0.79	18.36	21.83
HBC	A	12.26 (13)	0.55	11.49	13.65	**LD**	A	12.74 (13)	0.97	11.36	14.98
	R	12.44 (2)	0.25	12.26	12.62		R	13.56 (2)	0.47	13.22	13.89
	T	11.98 (34)	0.44	11.06	13.00		T	12.45 (34)	0.65	10.74	13.52
	M	11.94 (19)	0.31	11.53	12.67		M	12.22 (20)	0.66	10.97	13.18

Variable		mean	SD	Min.	Max	Variable		mean	SD	Min.	Max.
BZP	A	3.99 (13)	0.17	3.72	4.24	**LIF**	A	6.08 (13)	0.68	5.20	7.98
	R	4.55 (2)	0.30	4.34	4.76		R	5.96 (2)	0.06	5.91	6.00
	T	4.13 (34)	0.26	3.53	4.85		T	6.23 (34)	0.51	5.19	7.16
	M	4.15 (20)	0.41	3.54	5.20		M	5.93 (20)	0.48	4.99	6.59
LBP	A	8.61 (13)	0.34	8.07	9.13	**BIF**	A	3.81 (13)	0.28	3.19	4.25
	R	9.01 (2)	0.35	8.76	9.25		R	3.68 (2)	0.11	3.60	3.75
	T	8.25 (34)	0.48	7.22	9.07		T	3.61 (34)	0.27	3.05	4.19
	M	8.83 (20)	0.52	7.90	9.64		M	3.31 (20)	0.25	2.91	3.85
LB	A	4.98 (13)	0.18	4.71	5.27	**LM$^{1\text{-}3}$**	A	6.64 (13)	0.24	6.24	7.04
	R	4.91 (2)	0.20	4.77	5.05		R	6.53 (2)	0.06	6.49	6.57
	T	4.71 (34)	0.28	3.87	5.25		T	6.83 (34)	0.24	6.16	7.34
	M	4.81 (19)	0.33	4.06	5.24		M	6.48 (20)	0.27	5.83	6.98
PPL	A	16.99 (13)	0.73	15.69	18.27	**BM^{1}**	A	2.07 (13)	0.08	1.93	2.21
	R	17.01 (2)	0.37	16.84	17.36		R	1.94 (2)	0.04	1.91	1.97
	T	16.09 (34)	0.82	13.96	17.71		T	2.24 (34)	0.10	2.06	2.47
	M	15.60 (18)	0.60	14.55	16.90		M	2.11 (20)	0.09	1.91	2.20
PL	A	22.05 (13)	1.03	20.81	24.40	**LM**	A	23.04 (13)	0.90	21.24	24.55
	R	22.54 (2)	0.29	22.33	22.74		R	24.15 (2)	0.70	23.65	24.64
	T	21.72 (34)	0.89	19.28	23.43		T	22.81 (34)	0.92	19.88	25.02
	M	21.75 (20)	1.03	19.82	23.81		M	22.24 (19)	0.90	20.51	23.84
BMF	A	2.86 (13)	0.27	2.35	3.33	**HM**	A	11.12 (13)	0.54	10.27	12.12
	R	2.80 (2)	0.16	2.68	2.91		R	11.43 (2)	0.03	11.41	11.45
	T	2.94 (34)	0.17	2.50	3.28		T	11.03 (34)	0.64	8.87	12.09
	M	2.74 (19)	0.21	2.33	3.16		M	10.61 (19)	0.55	9.72	11.67
BAM	A	4.67 (13)	0.31	4.20	5.26	**LM$_{1\text{-}3}$**	A	6.60 (13)	021	6.16	6.89
	R	4.47 (2)	0.04	4.44	4.50		R	6.38 (2)	0.14	6.28	6.48
	T	4.92 (34)	0.33	3.98	5.49		T	6.81 (34)	0.20	6.46	7.12
	M	4.29 (19)	0.41	3.54	5.18		M	6.43 (19)	0.27	5.92	6.79

Appendix 2. One-way analysis of variance and individual comparisons (posthoc scheffe's) between pairs of samples for *M. surifer*. A: Adang; R: Rawi; T: Tarutao; and M: Mainland. '.': p=0.1; '*': p=0.05; '**': p=0.01; '***': p=0.001;'-' : p = 1 (no statistical significance).

Variable	df	*F* statistic	*P* value	r^2	Adj. r^2	A-R	A-T	A-M	R-T	R-M	T-M
HB	3,67	0.145	0.9328	0.006	-0.039	-	-	-	-	-	-
T	3,65	23.58	1.929e-10	0.521	0.499	-	***	***	-	*	**
E	3,67	0.029	0.9933	0.001	-0.043	-	-	-	-	-	-
HF	3,67	8.684	6.022e-05	0.28	0.248	-	-	*	-	-	***
GSL	3,63	5.058	0.0033	0.194	0.156	-	-	***	-	-	-
HBC	3,64	2.286	0.0872	0.097	0.054	-	-	-	-	-	-
BZP	3,65	2.349	0.0807	0.098	0.056	-	-	-	-	-	-
LR	3,64	5.637	0.0017	0.209	0.172	-	-	-	-	-	***
BR	3,65	1.886	0.1406	0.08	0.038	-	-	-	-	-	-
LN	3,64	2.935	0.04	0.121	0.08	-	-	-	-	-	*
IB	3,65	6.715	0.0005	0.237	0.201	-	***	***	-	-	-
BBC	3,65	3.785	0.0145	0.149	0.109	-	-	-	-	-	*
ZB	3,59	1.39	0.2546	0.066	0.019	-	-	-	-	-	-
LD	3,65	2.917	0.0407	0.119	0.078	-	-	-	-	-	-
LBP	3,65	7.397	0.0002	0.255	0.22	-	-	-	-	-	***
LB	3,64	3.284	0.0263	0.133	0.093	-	*	-	-	-	-
PPL	3,63	9.949	1.855e-05	0.322	0.289	-	**	***	-	.	-
PL	3,65	0.792	0.5029	0.035	-0.009	-	-	-	-	-	-
BMF	3,64	3.933	0.0122	0.156	0.116	-	-	-	-	-	*
BAM	3,64	13.67	5.417e-07	0.391	0.362	-	-	*	-	-	***
LIF	3,65	1.44	0.2392	0.062	0.019	-	-	-	-	-	-
BIF	3,65	10.31	1.226e-05	0.322	0.291	-	-	***	-	-	***
LM^{1-3}	3,65	9.166	3.846e-05	0.297	0.265	-	.	-	-	-	***
BM^1	3,65	18.29	1.031e-08	0.458	0.433	-	***	-	***	.	***
LM	3,64	4.088	0.0101	0.161	0.122	-	-	.	-	*	-
HM	3,64	2.996	0.0371	0.123	0.082	-	-	.	-	.	.
LM_{1-3}	3,64	13.37	7.084e-07	0.385	0.357	-	*	-	.	-	***

Appendix 3. Descriptive statistics of all external and cranial measurements of *R. tanezumi* from Adang (A), Rawi (R), Butong (B), Yang (Y), Tarutao (T), and Mainland (M) samples.

Variable		n	mean	SD	Min.	Max.	Variable		n	mean	SD	Min.	Max.
HB	A	6	174.82	5.84	165.84	181.70	**HBC**	A	5	11.65	0.30	11.28	12.05
	R	6	178.56	21.28	151.43	209.52		R	6	12.17	0.20	11.96	12.48
	B	3	186.08	9.87	175.13	194.32		B	2	12.04	0.40	11.75	12.32
	Y	7	150.77	5.86	142.17	159.66		Y	7	10.81	0.45	9.87	11.30
	T	32	159.00	13.12	132.30	195.60		T	30	11.65	0.54	10.63	12.86
	M	5	165.05	9.13	155.00	175.00		M	11	11.53	0.54	10.64	12.33
T	A	6	183.23	6.88	177.64	196.70	**BZP**	A	5	5.09	0.28	4.61	5.33
	R	6	182.28	10.61	173.43	199.98		R	6	5.63	0.35	5.18	6.11
	B	3	176.24	14.77	164.35	192.77		B	2	5.77	0.31	5.55	5.99
	Y	7	164.22	8.31	152.53	171.45		Y	7	4.27	0.28	3.91	4.74
	T	27	163.80	11.47	139.60	185.90		T	30	4.58	0.49	3.88	6.32
	M	5	177.37	16.15	159.61	197.00		M	11	4.65	0.35	4.08	5.12
E	A	6	25.00	1.63	22.82	27.00	**LR**	A	5	15.11	0.69	14.00	15.73
	R	6	24.37	1.60	22.17	27.08		R	6	14.43	0.59	13.86	15.21
	B	3	22.16	2.52	20.43	25.06		B	2	14.83	1.02	14.11	15.55
	Y	7	19.69	1.02	18.38	21.23		Y	7	12.77	0.52	12.00	13.46
	T	27	21.69	1.74	18.50	26.30		T	29	13.21	0.74	11.84	14.38
	M	5	21.09	1.57	19.31	22.80		M	11	13.21	0.82	11.73	14.75
HF	A	6	37.19	1.95	34.95	39.95	**BR**	A	5	8.42	0.26	8.02	8.67
	R	6	36.67	1.92	34.62	39.78		R	6	8.29	0.58	7.61	9.16
	B	3	36.44	0.93	35.76	37.50		B	2	7.93	0.30	7.72	8.14
	Y	7	34.59	1.54	32.45	36.82		Y	7	7.44	0.17	7.10	7.61
	T	32	33.99	1.86	29.20	37.70		T	30	7.25	0.42	6.19	8.03
	M	5	32.13	1.57	30.78	34.50		M	11	7.32	0.53	6.35	8.23

Variable		n	mean	SD.	Min.	Max.	Variable		n	mean	SD	Min.	Max.
GSL	A	5	45.54	1.62	42.96	47.38	**LN**	A	5	17.31	1.03	15.75	18.53
	R	6	44.90	1.14	43.58	46.22		R	6	17.20	0.18	16.50	17.57
	B	2	45.11	1.30	44.19	46.03		B	2	16.20	1.49	15.14	17.25
	Y	7	41.23	1.28	39.29	42.46		Y	7	15.54	0.77	14.41	16.37
	T	29	41.24	1.86	36.86	45.53		T	29	15.47	0.77	13.91	16.93
	M	11	41.37	146	38.82	43.61		M	11	15.08	0.89	13.71	16.88
IB	A	5	6.78	0.35	6.24	7.08	**LB**	A	5	7.26	0.25	6.94	7.57
	R	6	7.00	0.39	6.48	7.57		R	6	7.31	0.41	6.91	7.96
	B	2	7.01	0.26	6.82	7.19		B	2	7.56	0.16	7.45	7.67
	Y	7	6.83	0.26	6.33	7.17		Y	7	6.88	0.18	6.50	7.05
	T	30	6.45	0.25	5.78	7.03		T	10	6.82	0.32	6.13	7.44
	M	11	6.28	0.43	5.60	7.16		M	11	7.13	0.31	6.75	7.62
BBC	A	5	16.61	0.30	16.15	16.98	**PPL**	A	5	15.35	0.83	14.30	16.55
	R	6	16.24	0.47	15.52	16.81		R	6	15.28	0.49	14.64	15.91
	B	2	16.27	0.35	16.02	16.52		B	2	14.80	0.52	14.43	15.16
	Y	7	15.56	0.57	14.50	16.17		Y	7	13.71	0.48	13.05	14.34
	T	30	15.92	0.42	15.13	16.95		T	30	13.62	0.83	11.78	16.10
	M	11	16.09	0.59	15.09	16.88		M	11	14.05	0.70	12.80	15.30
ZB	A	5	22.31	0.65	21.24	23.00	**PL**	A	5	24.94	0.93	23.47	25.95
	R	6	21.31	0.52	20.55	22.05		R	6	25.24	0.91	24.10	26.59
	B	2	20.74	1.23	19.87	21.61		B	2	24.69	0.69	24.20	25.17
	Y	7	19.82	0.41	19.00	20.23		Y	7	22.67	0.60	21.55	23.41
	T	29	19.45	0.91	17.62	21.60		T	30	22.82	1.12	20.09	25.34
	M	11	19.95	1.17	18.06	21.96		M	11	22.55	1.10	21.08	24.41
LD	A	5	12.53	0.83	11.08	13.13	**BMF**	A	5	2.79	0.18	2.57	2.98
	R	6	12.52	0.64	12.00	13.62		R	6	2.87	0.33	2.36	3.24
	B	2	12.13	0.75	11.60	12.66		B	2	2.77	0.04	2.74	2.79
	Y	7	11.87	0.43	11.15	12.54		Y	7	2.40	0.21	2.21	2.76
	T	30	11.83	0.80	10.19	13.71		T	29	2.80	0.20	2.39	3.15
	M	11	11.43	0.71	10.31	12.68		M	10	2.63	0.16	2.43	2.95

Variable		n	mean	SD.	Min.	Max.	Variable		n	mean	SD	Min.	Max.
LBP	A	5	9.42	0.43	8.68	9.76	**BAM**	A	5	4.87	0.61	4.11	5.79
	R	6	9.41	0.44	8.86	10.10		R	6	4.61	0.42	4.13	5.39
	B	2	9.46	0.22	9.30	9.61		B	2	4.09	0.59	3.67	4.51
	Y	7	8.70	0.29	8.44	9.15		Y	7	4.35	0.22	4.08	4.64
	T	30	8.89	0.42	7.97	9.88		T	30	5.23	0.46	4.61	6.53
	M	11	8.33	0.69	7.24	9.44		M	11	5.35	0.56	4.53	6.41
LIF	A	5	7.94	0.29	7.54	8.24	**LM**	A	5	24.70	0.72	23.52	25.36
	R	6	8.43	0.57	8.01	9.53		R	6	24.95	0.73	23.60	25.66
	B	2	8.14	0.33	7.91	8.37		B	2	24.80	0.06	24.75	24.84
	Y	7	6.98	0.29	6.55	7.22		Y	7	21.19	0.55	20.36	22.09
	T	30	7.33	0.40	6.58	8.52		T	30	22.04	1.18	19.80	25.62
	M	11	7.44	0.55	6.32	8.24		M	11	21.54	1.20	19.95	23.41
BIF	A	5	3.33	0.17	3.10	3.52	**HM**	A	5	14.18	0.78	13.07	15.12
	R	6	3.11	0.30	2.68	3.46		R	6	14.83	0.93	13.34	15.82
	B	2	2.98	0.06	2.94	3.02		B	2	14.39	0.59	13.97	14.80
	Y	7	2.62	0.20	2.31	2.87		Y	7	12.20	0.47	11.41	12.77
	T	30	2.83	0.20	2.49	3.36		T	30	12.19	0.76	10.75	13.56
	M	11	2.64	0.21	2.40	3.13		M	11	12.14	0.82	10.42	13.39
LM$^{1-3}$	A	5	7.34	0.23	7.02	7.61	**LM$_{1-3}$**	A	5	7.39	0.11	7.29	7.55
	R	6	7.65	0.11	7.48	7.78		R	6	7.25	0.37	6.53	7.61
	B	2	7.26	0.09	7.19	7.32		B	2	7.08	0.27	6.89	7.27
	Y	7	6.16	0.09	6.05	6.33		Y	7	6.12	0.17	5.85	6.40
	T	30	6.58	0.21	6.19	7.00		T	30	6.54	0.23	6.22	7.04
	M	11	6.53	0.37	6.01	7.31		M	11	6.45	0.33	5.85	7.05
BM^{1}	A	5	2.30	0.04	2.23	2.34							
	R	6	2.20	0.11	2.06	2.32							
	B	2	2.26	0.02	2.24	2.27							
	Y	7	1.85	0.07	1.78	1.99							
	T	30	2.08	0.09	1.85	2.23							
	M	11	1.99	0.13	1.85	2.30							

Appendix 4. Results of analysis of variance and individual posthoc scheffe's comparisons between pairs of samples. A: Adang; R: Rawi; T: Tarutao; and M: Mainland. '.': p=0.1; '*': p=0.05; '**': p=0.01; '***': p=0.001; - : p = 1 (no statistical significance).

Variable	df	*F* statistic	*P* value	r^2	Adj. r^2	A-R	A-B	A-Y	A-T	A-M	R-B	R-Y	R-T	R-M	B-Y	B-T	B-M	Y-T	Y-M	T-M
HB	5,53	6.80	5.817e-05	0.391	0.333	-	-	*	.	-	-	**	*	-	***	*	-	-	-	-
T	5,48	5.67	3.453e-04	0.371	0.306	-	-	.	*	-	-	.	*	-	-	-	-	-	-	-
E	5,53	9.42	1.814e-06	0.471	0.421	-	-	***	***	*	-	***	*	.	-	-	-	-	-	-
HF	5,53	7.38	2.592e-05	0.41	0.355	-	-	-	**	***	-	-	.	**	-	-	.	-	-	-
GSL	5,54	11.56	1.289e-07	0.517	0.472	-	-	***	***	***	-	**	***	**	.	.	.	-	-	-
HBC	5,55	5.72	2.576e-04	0.342	0.282	-	-	.	-	-	-	***	-	-	.	-	-	**	.	-
BZP	5,55	11.05	2.14e-07	0.501	0.456	-	-	.	-	-	-	***	***	***	***	**	*	-	-	-
LR	5,54	11	2.468e-07	0.505	0.459	-	-	***	***	***	-	**	*	.	*	.	-	-	-	-
BR	5,55	11.44	1.359e-07	0.51	0.465	-	-	*	***	***	-	*	***	***	-	-	-	-	-	-
LN	5,54	9.94	8.841e-07	0.48	0.431	-	-	*	***	***	-	*	***	***	-	-	-	-	-	-
IB	5,55	7.04	3.8e-05	0.39	0.335	-	-	-	-	.	-	-	*	***	-	-	.	-	*	-
BBC	5,55	3.61	0.0068	0.247	0.179	-	-	*	.	-	-	-	-	-	-	-	-	-	-	-
ZB	5,54	11.92	8.585e-08	0.525	0.481	-	-	***	***	***	-	.	***	.	-	-	-	-	-	-
LD	5,55	2.53	0.0396	0.187	0.113	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LBP	5,55	6.75	5.749e-05	0.38	0.324	-	-	-	-	**	-	-	-	***	-	-	.	-	-	*
LB	5,55	5.97	1.769e-04	0.352	0.293	-	-	-	.	-	-	-	*	-	-	.	-	-	-	-

Variable	df	*F* statistic	*P* value	r^2	Adj. r^2	A-R	A-B	A-Y	A-T	A-M	R-B	R-Y	R-T	R-M	B-Y	B-T	B-M	Y-T	Y-M	T-M
PPL	5,55	9	2.712e-06	0.45	0.4	-	-	*	***	.	-	*	***	.	-	-	-	-	-	-
PL	5,55	10.37	4.852e-07	0.485	0.439	-	-	*	**	**	-	***	***	***	-	-	-	-	-	-
BMF	5,53	5.49	3.85e-04	0.341	0.279	-	-	.	-	-	-	**	-	-	-	-	-	***	-	-
BAM	5,55	7.64	1.642e-05	0.41	0.356	-	-	-	-	-	-	-	.	.	-	.	*	***	**	-
LIF	5,55	10.44	4.439e-07	0.487	0.44	-	-	*	-	-	-	***	***	***	.	-	-	-	-	-
BIF	5,55	11.33	1.546e-07	0.507	0.463	-	-	***	***	***	-	**	.	***	-	-	-	-	-	-
LM$^{1-3}$	5,55	39.67	<2.2e-16	0.783	0.763	-	-	***	***	***	-	***	***	***	***	*	**	**	.	-
BM^{1}	5,55	17.96	1.604e-10	0.62	0.586	-	-	***	***	***	-	***	-	**	***	-	*	***	.	-
LM	5,55	17.75	1.952e-10	0.617	0.583	-	-	***	***	***	-	***	***	***	**	*	**	-	-	-
HM	5,55	19.66	3.508e-11	0.641	0.609	-	-	***	***	***	-	***	***	***	*	*	*	-	-	-
LM$_{1-3}$	5,55	24.51	6.869e-13	0.69	0.662	-	-	***	***	***	-	***	***	***	***	-	.	*	-	-

Appendix 5. Variable coefficients, eigenvalues and % of variance explained by the first three principle components (PC1-PC3) performed based on 10 skull measurements of *M. surifer* specimens. The uppercase asterisks (*) stresses the variables that contributed the greatest percentage of variation on each principle component (PC).

Variable	PC1	PC2	PC3
GSL	-13.3272*	1.3170	-0.5896
LR	-6.8108*	-3.7940*	-0.9421
IB	-1.3966	0.7156	1.2009
LBP	-1.2536	2.4673*	-2.3138*
PPL	-5.9232*	1.6719	2.0730*
BAM	-2.1824	-1.8159	0.8147
BIF	-1.5126	-0.2564	1.0755
LM^{1-3}	-0.7634	-1.0549	-0.2112
BM^{1}	-0.0184	-0.5575	-0.1236
LM_{1-3}	-0.4947	-1.0925	-0.0450
Eigenvalue	270.485	31.504	14.211
% of Variance	78.424	9.134	4.120

Appendix 6. Eigenvectors, eigenvalues and % of variance explained by the first three principle components (PC1-PC3) performed based on 8 skull measurements of *R. tanezumi* specimens. The uppercase asterisks (*) on the eigenvectors stresses the variables that contributed the greatest percentage of variation on each principle component (PC).

Variable	PC1	PC2	PC3
GSL	-17.1603*	-1.7005	-0.3126
LR	-6.5693	-2.2165*	0.1941
LN	-7.2784	-1.8255	2.3238*
ZB	-8.4880	-0.0039	-2.8216*
PPL	-6.6544	0.2531	-1.7550
PL	-10.3272*	0.6634	0.7511
LM	-11.8881*	3.3534*	1.1827
HM	-8.8297	0.9808	0.1118
Eigenvalue	832.877	23.849	18.552
% of Variance	90.107	2.580	2.007

APPENDIX 7. Cytochrome *b* gene nucleotide sequences for both *R. tanezumi* (RT) and *M. surifer* (MS) analyzed in chapter 4. Showing both the names from BOLD and the abbreviation used in this study are given in brackets.

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AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT

CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA049-13|IC130112.6|Maxomys surifer|CYTB (MS Tarutao4)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGTCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA050-13|IC130106.2|Maxomys surifer|CYTB (MS Tarutao5)

GAAACTTTGGCTCTCTCTTAGGCATATGCCTAATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGA
GATGTAAATTACGGCTGACTAATCCGATATATACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAAC
CTGAAACATTGGAGTCATCCTCCTATTTGCAGTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTA
TTCCATATATCGGAACCACCCTAGTCGAATGAATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCA
ATTGTTCACCTCTTATTTCTTCACGAAACAGGCTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCAT
CCTAATTCTCTTCCTAATGACTTTAGTCCTATTCTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTA-------------------------------------
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>RTSEA052-13|IC130114.7|Maxomys surifer|CYTB (MS Tarutao6)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTCCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCATACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA053-13|IC130114.8|Maxomys surifer|CYTB (MS Tarutao7)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCATAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA054-13|IC130113.3|Maxomys surifer|CYTB (MS Tarutao8)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGTTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA055-13|IC130109.1|Maxomys surifer|CYTB (MS Tarutao9)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCA--
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>RTSEA056-13|IC130110.4|Maxomys surifer|CYTB (MS Tarutao10)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG

CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA057-13|IC130109.4|Maxomys surifer|CYTB (MS Tarutao11)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCACAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTTCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA058-13|IC130105.8|Maxomys surifer|CYTB (MS Tarutao12)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTA--
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>RTSEA059-13|IC130105.7|Maxomys surifer|CYTB (MS Tarutao13)

GAAACTTTGGCTCTCTCTTAGGCATATGCCTAATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGA
GATGTAAATTACGGCTGACTAATCCGATATATACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAAC
CTGAAACATTGGAGTCATCCTCCTATTTGCAGTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTA
TTCCATATATCGGAACCACCCTAGTCGAATGAATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCA
ATTGTTCACCTCTTATTTCTTCACGAAACAGGCTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCAT
CCTAATTCTCTTCCTAATGACTTTAGTCCTATTCTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCA---------------------------
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>RTSEA060-13|IC130105.11|Maxomys surifer|CYTB (MS Tarutao14)

ATGACAAACATCCGAAAAACCCATCCCTTATTCAAAATCATCAACCACTCCTTCATTGACCTTCCCACCCCATCTAACATCTCATCATGATGAAACTTTGGCTCTCTCTTAGGCATATGCCT
AATTATTCAAATTATTACAGGCCTATTCCTAGCAATACATTACACATCCGACACTATAACAGCATTCTCATCAGTAACACATATCTGCCGAGATGTAAATTACGGCTGACTAATCCGATATA
TACATGCAAATGGGGCCTCCATATTTTTCATCTGCTTGTTCTTACATGTAGGACGAGGCATATACTATGGATCCTATACCTTCATAGAAACCTGAAACATTGGAGTCATCCTCCTATTTGCA
GTTATAGCAACCGCATTCATAGGCTACGTACTCCCATGAGGACAAATATCATTCTGAGGTGCAACAGTAATTACAAATCTTTTATCAGCTATTCCATATATCGGAACCACCCTAGTCGAATG
AATCTGAGGCGGCTTCTCAGTAGATAAAGCCACCCTAACACGATTTTTCGCATTCCACTTCATCCTTCCATTTATCATCGCAGCCCTCGCAATTGTTCACCTCTTATTTCTTCACGAAACAGG
CTCCAACAATCCCACAGGCCTAGACTCAGACGCAGACAAAATCCCCTTCCACCCTTATTACACTATCAAAGACCTCCTAGGAATCTTCATCCTAATTCTCTTCCTAATGACTTTAGTCCTATT
CTTCCCAGACCTACTAGGAGACCCAGACAACTACACCCCCGCAAATCCCCTAAACACACCACCCCACATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGTTCCATTCCAA
ACAAACTAGGAGGAGTCGTAGCCTTAGTCTTATCCATCCTAATCCTAGCCTTCCTACCATTCCTCCACACATCAAAACAACGAAGCCTCACCTTCCGCCCAATCACCCAAATCCTCTACTGA
ATCCTAGTAGCTAACCTCCTCATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCATTCATTATCATCGGACAACTAGCATCCATCAGCTACTTCTCAATTATCCTCATCCTCATACC
CCTCTCAGGAATAATCGAAGACAAAATACTAAAATGAAAT

>RTSEA028-13|IC130112.3|Rattus tanezumi|CYTB (RT Tarutao1)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT

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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGAGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA029-13|IC130110.1|Rattus tanezumi|CYTB (RT Tarutao2)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA030-13|IC130114.2|Rattus tanezumi|CYTB (RT Tarutao3)

ATGACAAACATCCGGAAATCACACCCCCTACTTAAAATCATTAATCACGCCTTCATCGACCTCCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATCCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGATGTAAACTACGGCTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTTGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATCACAAACCTATTATCAGCTATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
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GATCAAACAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCACCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATGTCTGATAACTCTAGTACT
ATTCTTTCCAGACTCACTAGGAGACCCAGACAATTACACACCTGCTAATCCACTAAACACCCCACCACATATTAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCTATCC
CCAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTTTAATCCTAGCCTTCCTACCATTCCTACATACCTCAAAACAACGTAGTCTAACATTCCGCCCAATCACCCAAACCCTATAC
TGAATTCTAGTAGCCAACCTCTTCATTTTAACATGAATCGGAGGCCAACCAGTAGAACACCCATTTATTATCATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATA
CCAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA031-13|IC130114.10|Rattus tanezumi|CYTB (RT Tarutao4)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA032-13|IC130114.11|Rattus tanezumi|CYTB (RT Tarutao5)

GAAATTTTGGCTCTCTACTAGGAGTATGCCTCATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTCACCCACATCTGCCGA
GACGTAAACTACGGTTGATTAATCCGATACTTACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAAC
ATGAAACATTGGAGTCGTCCTACTATTTGCAGTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCC
ATTCCCTACATTGGTACCACCCTAGTCGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCA
ATTGTACATCTCCTCTTCCTCCACGAAACAGGATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCAT
TCTACTCCTATGTCTGATAACTCTAGTATTATTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCC
TATTTGCCTACGCTATTCTACGCTCCATCCCCAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAA

TATTCCGCCCAATCACCCAAACCCTATACTGAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATC
AGTTACTTCTCAATTATCCTTATCCTAATACCAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA033-13|IC130107.8|Rattus tanezumi|CYTB (RT Tarutao46)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGAGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA023-13|IC130107.4|Rattus tanezumi|CYTB (RT Tarutao7)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGAGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA002-13|UP100808.2|Rattus tanezumi|CYTB (RT Trang)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
TATAGTTCAAATTATCACAGGCCTATTCCTAGCAATACATTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTATGGATGACTAATCCGATACT
TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTGTTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGGGGGGCCACAGTAATCACAAACCTATTATCAGCTATTCCCTATATTGGCACCACCCTAGTCGAATGA
ATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGGA
TCAAACAACCCCACAGGACTAAACTCTGACGCAGACAAAATCCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATATTACTCCTATTTCTAATAACTCTAGTATTATT
TTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATTCTACGCTCCATCCCTA
ACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTGA
ATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATCAGTTACTTCTCGATTATCCTTATTCTAATACCA
ATTTCCGGAATCATTGAAGACAAAATACTAAAATGAAAC

>RTSEA003-13|UP100723.3|Rattus tanezumi|CYTB (RT Songkhla)

ATGACAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA004-13|IC120317.16|Rattus tanezumi|CYTB (RT Yang1)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA005-13|IC120317.14|Rattus tanezumi|CYTB (RT Yang2)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA006-13|IC120317.19|Rattus tanezumi|CYTB (RT Yang3)

ATGGCAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCACCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
CATAATTCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCCGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTACGGTTGATTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA

GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
GATCAAACAATCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATTCTACTCCTATGTCTGATAACTCTAGTATTA
TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATCAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
CAATAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTTCTACATACTTCAAAACAACGTAGTCTAATATTCCGCCCAATCACCCAAACCCTATACT
GAATTCTAGTAGCTAACCTCTTCATTTTAACATGAATCGGGGGCCAACCAGTAGAGCACCCATTTATTATTATTGGCCAACTAGCATCCATCAGTTACTTCTCAATTATCCTTATCCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>RTSEA007-13|IC120318.2|Rattus tanezumi|CYTB (RT Adang1)

ATGACAAACATTCGGAAATCACACCCCCTACTCAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTGGGAGTATGCCT
CATAGTCCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCTGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTGAACTACGGCTGGCTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCCTATTCCTTCATGTAGGACGAGGTATATACTACGGATCCTACACTTTCCTAGAAACATGAAATATTGGAGTCGTTCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATCCCCTATATTGGCACTACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
GATCAAATAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATTTCTAATAACTCTAGTATTA
TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCATTAAATACCCCACCACATATTAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCAATCCC
CAATAAACTAGGAGGGGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTCCTACATACTTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACCCTATACT
GAATCCTAGTGGCCAATCTCTTCATTTTAACATGAATCGGAGGACAACCAGTAGAACATCCATTTATTATTATTGGCCAACTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAT

>RTSEA008-13|IC120320.12|Rattus tanezumi|CYTB (RT Adang2)

ATGACAAACATTCGGAAATCACACCCCCTACTCAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTGGGAGTATGCCT
CATAGTCCAAATTATCACAGGCCTATTCCTAGCAATACACTACACATCTGACACTTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTGAACTACGGCTGGCTAATCCGATACT
TACATGCCAACGGAGCTTCAATATTCTTTATCTGCCTATTCCTTCATGTAGGACGAGGTATATACTACGGATCCTACACTTTCCTAGAAACATGAAATATTGGAGTCGTTCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATCCCCTATATTGGCACTACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
GATCAAATAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATTTCTAATAACTCTAGTATTA

TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCATTAAATACCCCACCACATATTAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCAATCCC
CAATAAACTAGGAGGGGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTCCTACATACTTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACCCTATACT
GAATCCTAGTGGCCAATCTCTTCATTTTAACATGAATCGGAGGACAACCAGTAGAACATCCATTTATTATTATTGGCCAACTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAT

>RTSEA009-13|IC120317.18|Rattus tanezumi|CYTB (RT Adang3)

ATGACAAACATTCGGAAATCACACCCCCTACTCAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTGGGAGTATGCCT
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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCCTATTCCTTCATGTAGGACGAGGTATATACTACGGATCCTACACTTTCCTAGAAACATGAAATATTGGAGTCGTTCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATCCCCTATATTGGCACTACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
GATCAAATAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATTTCTAATAACTCTAGTATTA
TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCATTAAATACCCCACCACATATTAAACCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCAATCCC
CAATAAACTAGGAGGGGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTCCTACATACTTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACCCTATACT
GAATCCTAGTGGCCAATCTCTTCATTTTAACATGAATCGGAGGACAACCAGTAGAACATCCATTTATTATTATTGGCCAACTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAT

>RTSEA010-13|IC120320.11|Rattus tanezumi|CYTB (RT Adang4)

ATGACAAACATTCGGAAATCACACCCCCTACTCAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTGGGAGTATGCCT
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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCCTATTCCTTCATGTAGGACGAGGTATATACTACGGATCCTACACTTTCCTAGAAACATGAAATATTGGAGTCGTTCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATCCCCTATATTGGCACTACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
GATCAAATAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATTTCTAATAACTCTAGTATTA
TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCATTAAATACCCCACCACATATTAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCAATCCC
CAATAAACTAGGAGGGGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTCCTACATACTTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACCCTATACT

GAATCCTAGTGGCCAATCTCTTCATTTTAACATGAATCGGAGGACAACCAGTAGAACATCCATTTATTATTATTGGCCAACTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAT

>RTSEA011-13|IC120317.1|Rattus tanezumi|CYTB (RT Adang5)

ATGACAAACATTCGGAAATCACACCCCCTACTCAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTGGGAGTATGCCT
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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCCTATTCCTTCATGTAGGACGAGGTATATACTACGGATCCTACACTTTCCTAGAAACATGAAATATTGGAGTCGTTCTACTATTTGCA
GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATCCCCTATATTGGCACTACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
GATCAAATAACCCCACAGGACTAAACTCTGACGCAGACAAAATTCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATACTACTCCTATTTCTAATAACTCTAGTATTA
TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCATTAAATACCCCACCACATATTAAGCCAGAATGATATTTCCTATTTGCCTACGCTATTCTACGCTCAATCCC
CAATAAACTAGGAGGGGTAGTAGCCTTAGTCCTATCAATTCTAATCCTAGCCTTCCTACCATTCCTACATACTTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACCCTATACT
GAATCCTAGTGGCCAATCTCTTCATTTTAACATGAATCGGAGGACAACCAGTAGAACATCCATTTATTATTATTGGCCAACTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATAC
CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAT

>RTSEA012-13|IC120318.121|Rattus tanezumi|CYTB (RT Rawi1)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
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TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCTATCCCCTATATTGGCACCACCCTAGTCGAATG
AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
ATCAAACAACCCCACAGGACTAAACTCTGACGCAGACAAAATCCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATATTACTCCTATTTCTGATAACTCTAGTATTAT
TTTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATCCTACGCTCCATCCCT
AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
AATTTCCGGAATCATTGAAGACAAAATACTAAAATGAAAC

>RTSEA013-13|IC120317.20|Rattus tanezumi|CYTB (RT Rawi2)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
TATAATTCAAATTATCACAGGCCTATTCCTAGCAATACATTACACATCCGACACCTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTATGGGTGACTAATCCGATACT
TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCTATCCCCTATATTGGCACCACCCTAGTCGAATG
AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
ATCAAACAACCCCACAGGACTAAACTCTGACGCAGACAAAATCCCATTTCATCCATACTACACAATTAAAGACCTACTTGGAGTATTCATATTACTCCTATTTCTGATAACTCTAGTATTAT
TTTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATCCTACGCTCCATCCCT
AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
AATTTCCGGAATCATTGAAGACAAAATACTAAAATGAAAC

>RTSEA014-13|IC120318.10|Rattus tanezumi|CYTB (RT Rawi3)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
TATAATTCAAATTATCACAGGCCTATTCCTAGCAATACATTACACATCCGACACCTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTATGGGTGACTAATCCGATACT
TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCTATCCCCTATATTGGCACCACCCTAGTCGAATG
AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
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TTTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATCCTACGCTCCATCCCT
AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
AATTTCCGGAATCATTGAAGACAAAATACTAAAATGAAAC

>RTSEA015-13|IC120318.12|Rattus tanezumi|CYTB (RT Rawi4)

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TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
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AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
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TTTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATCCTACGCTCCATCCCT
AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
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>RTSEA016-13|IC120216.3|Rattus tanezumi|CYTB (RT Rawi5)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
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TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCTATCCCCTATATTGGCACCACCCTAGTCGAATG
AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
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TTTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCACTAAATACCCCACCACATATTAAGCCAGAATGATACTTCCTATTTGCCTACGCTATCCTACGCTCCATCCCT
AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
AATTTCCGGAATCATTGAAGACAAAATACTAAAATGAAAC

>RTSEA017-13|IC120213.14|Rattus tanezumi|CYTB (RT Butong1)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
TATAATTCAAATTATCACAGGCCTATTCCTAGCAATACATTACACATCCGACACCTTAACAGCATTCTCATCAGTTACCCACATCTGCCGAGACGTAAACTATGGGTGACTAATCCGATACT
TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG

TCATAGCAACCGCATTCATAGGTTATGTACTTCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCTATCCCCTATATTGGCACCACCCTAGTCGAATG
AATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTTGCATTCCACTTCATCCTCCCATTTATCATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAGG
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AACAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTAGCCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTG
AATTCTAGTAGCCAACCTCTTCATCTTAACATGAATTGGAGGCCAACCAGTAGAACACCCATTTATTATTATTGGCCAACTAGCATCTATTAGTTATTTCTCGATTATCCTTATTCTAATACC
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>RTSEA018-13|IC120215.6|Rattus tanezumi|CYTB (RT Butong2)

ATGACAAACATTCGGAAATCACACCCCCTACTAAAAATCATTAACCACTCCTTCATTGATCTTCCAGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTTCTAGGAGTATGCCT
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TACATGCCAATGGAGCCTCAATATTCTTTATCTGTTTATTCCTCCATGTAGGCCGAGGGATATACTACGGATCCTACACCTTTTTAGAAACATGAAACATTGGAGTTGTCCTATTATTTGCAG
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A?CAAACTAGGAGGAGTAGTAGCCTTAGTCCTATCAATTCTAATCTTA?CCTTTCTACCATTCTTACATACCTCAAAACAACGCAGTCTAACATTCCGCCCAATCACCCAAACTCTATACTGA
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>RTSEA019-13|IC130107.12|Rattus tanezumi|CYTB (RT Tarutao8)

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GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATTACAAACCTATTATCAGCCATCCCCTATATTGGCACCACCCTAGTCGAAT
GAATCTGAGGAGGTTTCTCAGTAGACAAAGCAACCCTAACACGCTTTTTCGCATTCCACTTCATCCTCCCATTCATCATCGCCGCCCTTGCAATCGTACATCTCCTCTTCCTCCATGAAACAG
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TTCTTCCCAGACCTACTAGGAGACCCAGACAATTACACACCTGCTAATCCACTAAATACCCCACCACATATTAAGCCAGAATGGTATTTCCTATTTGCCTACGCTATTCTACGCTCCATCCC
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GAATCCTAGTAGCCAATCTCTTCATTTTAACATGAATCGGAGGACAGCCAGTAGAACATCCATTTATTATCACTGGCCAGCTAGCATCCATCAGCTACTTCTCAATTATCCTTATTCTAATA
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>RTSEA020-13|IC130106.5|Rattus tanezumi|CYTB (RT Tarutao9)

ATGACAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
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TTCTTCCCAGACTTACTAGGAGACCCAGACAATTACACACCTGCTAACCCATTAAACACCCCACCACATATTAA---------------------------------------------------------------------------------------------
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>RTSEA021-13|IC130107.7|Rattus tanezumi|CYTB (RT Tarutao10)

ATGACAAACATCCGAAAATCACACCCCCTACTTAAAATCATTAATCACTCCTTCATCGACCTTCCCGCCCCATCCAACATCTCATCATGATGAAATTTTGGCTCTCTACTAGGAGTATGCCT
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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
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GAATCTGAGGAGGCTTCTCAGTAGACAAAGCAACCCTAACACGTTTTTTCGCATTCCACTTCATCCTCCCATTCATTATCGCCGCCCTTGCAATTGTACATCTCCTCTTCCTCCACGAAACAG
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>RTSEA022-13|IC130107.5|Rattus tanezumi|CYTB (RT Tarutao11)
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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
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>RTSEA001-13|UP110819.5|Rattus tanezumi|CYTB (RT Chumphon)

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>RTSEA024-13|IC130113.4|Rattus tanezumi|CYTB (RT Tarutao12)

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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA

GTCATAGCAACTGCATTCATAGGCTATGTACTCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACAAACCTATTATCAGCCATTCCCTACATTGGTACCACCCTAGTCGAAT
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>RTSEA025-13|IC130107.9|Rattus tanezumi|CYTB (RT Tarutao13)

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>RTSEA026-13|IC130105.12|Rattus tanezumi|CYTB (RT Tarutao14)

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TACATGCCAACGGAGCTTCAATATTCTTTATCTGCTTATTCCTCCATGTAGGCCGAGGAATATACTACGGATCCTACACTTTCCTAGAAACATGAAACATTGGAGTCGTCCTACTATTTGCA
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>RTSEA027-13|IC130110.5|Rattus tanezumi|CYTB (RT Tarutao15)

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CAATCTCCGGAATTATCGAAGACAAAATACTGAAATGAAAC

>gi|299779223|gb|HM217360.1| Micromys minutus voucher BZ02 cytochrome b (cytb) gene partial cds mitochondrial (outgroup)

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TCTCTGTTGATAAAGCAACCTTAACACGATTTTTCGCATTTCACTTCATCTTGCCCTTCATCATTGCAGCTCTAGCAATCGTACATCTATTATTCCTTCACGAAACAGGTTCAAACAACCCAA
CAGGCCTAAATTCAGATGCAGACAAAATCCCATTCCACCCTTACTATACAATTAAAGACCTACTAGGTATTGCCCTCATGCTACTCTTCCTGATATCCCTAGTCTTATTCTCTCCTGACCTTT
TAGGAGATCCTGACAACTATATACCTGCAAACCCACTCAACACCCCTCCCCACATTAAACCAGAATGATATTTTCTTTTTGCTTATGCAATTCTTCGCTCAATCCCCAACAAACTAGGAGGA
GTTATTGCTCTAGTCCTCTCAATCCTAATTCTAGCCCTAATACCTTTATTACATACATCAAAACAACGAAGCCTAATATTCCGCCCAATCTCCCAAACACTATACTGAATTCTAGTAGCCAAT

CTCCTTATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCCTTTATTATCATTGGCCAACTAGCTTCTATTAGTTACTTCACAATCATCTTAGTTCTAATACCCATCTCAGGAATTATC
GAAGACAAA---------------

>gi|299779225|gb|HM217361.1| Micromys minutus voucher BZ07 cytochrome b (cytb) gene partial cds mitochondrial (outgroup)

ATCCGAAAAACCCACCCCTTAATAAAAATTATTAACCACTCCTTCATCGACCTCCCAGCTCCATCAAACATCTCATCATGATGAAATTTCGGCTCCCTCCTAGGAGTTTGCCTCATTGTGCA
AATTATCACAGGCCTATTTCTAGCTATACACTATACATCAGATACTATAACAGCATTCTCATCAGTCACTCATATCTGCCGAGATGTAAACTATGGCTGACTAATTCGATACATACATGCAA
ACGGCGCATCCATATTCTTCATCTGCTTATTCCTCCACGTAGGTCGTGGTATCTACTATGGATCCTATGCTTTCCTAGAAACATGAAACATCGGGGTAATCCTACTATTTGCAGTTATAGCAA
CCGCATTCATAGGATATGTACTTCCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATTACTAACCTCTTATCAGCAATCCCATATGTAGGAACAACCCTAGTAGAGTGAATCTGAGG
GGGTTTCTCTGTTGATAAAGCAACCTTAACACGATTTTTCGCATTTCACTTCATCTTGCCCTTCATCATTGCAGCTCTAGCAATCGTACATCTATTATTCCTTCACGAAACAGGTTCAAACAA
CCCAACAGGCCTAAATTCAGATGCAGACAAAATCCCATTCCACCCTTACTATACAATTAAAGACCTACTAGGTATTGCCCTCATGCTACTCTTCCTGATATCCCTAGTCTTATTCTCTCCTGA
CCTTTTAGGAGATCCTGACAACTATATACCTGCAAACCCACTCAACACCCCTCCCCACATTAAACCAGAATGATATTTTCTTTTTGCTTATGCAATTCTTCGCTCAATCCCCAACAAACTAG
GAGGAGTTATTGCTCTAGTCCTCTCAATCCTAATTCTAGCCCTAATACCTTTATTACATACATCAAAACAACGAAGCCTAATATTCCGCCCAATCTCCCAAACACTATACTGAATTCTAGTA
GCCAATCTCCTTATCCTAACATGAATCGGAGGCCAACCAGTAGAACATCCCTTTATTATCATTGGCCAACTAGCTTCTATTAGTTACTTCACAATCATCTTAGTTCTAATACCCATCTCAGGA
ATTATCGAAGACAAAATAT-----------

APPENDIX 8. Cytochrome oxidase 1 (CO1) gene nucleotide sequences for both *R. tanezumi* (RT) and *M. surifer* (MS) analyzed in chapter 4. Showing both the names from BOLD and the abbreviation used in this study are given in brackets.

>RTSEA035-13|UP110823.37|Maxomys surifer|COI-5P (MS Songkhla2)

ACCCTTTACTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTATAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATCGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCCATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCTCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCTGCCATAACCCAATA
CCAAACACCCTTATTTGTATGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTATTAACTGATCGAAACCTAAATACAACTTTCTTT
GACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA036-13|UP110823.40|Maxomys surifer|COI-5P (MS Songkhla3)

ACCCTTTACTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTATAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATCGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCCATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCTCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCTGCCATAACCCAATA
CCAAACACCCTTATTTGTATGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTATTAACTGATCGAAACCTAAATACAACTTTCTTT
GACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA037-13|UP110823.36|Maxomys surifer|COI-5P (MS Songkhla4)

ACCCTTTACTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTATAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATCGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCCATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACTTAACTATTTTCTCTCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCTGCCATAACCCAATA

CCAAACACCCTTATTTGTATGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTATTAACTGATCGAAACCTAAATACAACTTTCTTT
GACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA039-13|IC120215.8|Maxomys surifer|COI-5P (MS Rawi1)

AACCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCTGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA040-13|IC120319.11|Maxomys surifer|COI-5P (MS Rawi2)

ACCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCTGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA041-13|IC120319.4|Maxomys surifer|COI-5P (MS Adang1)

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CCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCAT
TGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAA
ACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCAT
GCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATAC

CAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTT
GACCCTGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA042-13|IC120319.3|Maxomys surifer|COI-5P (MS Adang2)

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GTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAA
CAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCATG
CAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATACC
AAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTG
ACCCTGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA043-13|IC120318.4|Maxomys surifer|COI-5P (MS Adang3)

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GTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAA
CAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCATG
CAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATACC
AAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTG
ACCCTGCAGGAGGTGGAGACCCTATTTTCTACCAACATCTATTT

>RTSEA044-13|IC120320.9|Maxomys surifer|COI-5P (MS Adang4)

ACCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATA

CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCTGCAGGAGGTGGAGAC-----------------------

>RTSEA045-13|IC120319.9|Maxomys surifer|COI-5P (MS Adang5)

----TTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCATTGT
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ATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCCGGCAACTTAGCTCATGCA
GGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAACATAAAACCACCCGCCATAACCCAATACCAA
ACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTGAC
CCTGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA047-13|IC130106.3|Maxomys surifer|COI-5P (MS Tarutao2)

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TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA048-13|IC130113.5|Maxomys surifer|COI-5P (MS Tarutao3)

ACCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA

CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA049-13|IC130112.6|Maxomys surifer|COI-5P (MS Tarutao4)

ACCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTGCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA051-13|IC130114.5|Maxomys surifer|COI-5P (MS Tarutao15)

ATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCATTGTCAC
AGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAACAATA
TAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCATGCAGGC
GCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATACCAAACA
CCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTGACCCCG
CAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA052-13|IC130114.7|Maxomys surifer|COI-5P (MS Tarutao6)

ACCCTTTATTTACTGTTCGGAACCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA

CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTACTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA053-13|IC130114.8|Maxomys surifer|COI-5P (MS Tarutao7)

AACCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
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AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA054-13|IC130113.3|Maxomys surifer|COI-5P (MS Tarutao8)

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CCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCATT
GTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAA
CAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCATG
CAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATACC
AAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTG
ACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA055-13|IC130109.1|Maxomys surifer|COI-5P (MS Tarutao9)

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TATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCATGCAG
GCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGCGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATACCAAA

CACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTGACCC
CGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA056-13|IC130110.4|Maxomys surifer|COI-5P (MS Tarutao10)

TTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCATTGT
CACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAACA
ATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCATGCA
GGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATACCAA
ACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTTTGAC
CCCGCAGGAGGTGGAGACCCTATTTTCTACCAACATCTATTT

>RTSEA057-13|IC130109.4|Maxomys surifer|COI-5P (MS Tarutao11)

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CCCTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCATT
GTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATAAA
CAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCATG
CAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATACC
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>RTSEA058-13|IC130105.8|Maxomys surifer|COI-5P (MS Tarutao12)

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AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA

CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA059-13|IC130105.7|Maxomys surifer|COI-5P (MS Tarutao13)

ACCCTTTATTTACTGTTCGGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA060-13|IC130105.11|Maxomys surifer|COI-5P (MS Tarutao14)

ACCCTTTATTTACTGTTCTGAGCCTGAGCAGGAATAGTAGGAACAGCTTTAAGCATCCTAATCCGAGCTGAATTAGGACAACCAGGGGCTCTTCTAGGCGATGATCAAATTTACAATGTCA
TTGTCACAGCCCATGCATTCGTAATAATTTTCTTCATAGTTATACCAATAATAATTGGAGGCTTTGGAAACTGACTTGTCCCCCTAATAATCGGAGCCCCTGATATAGCATTTCCACGAATA
AACAATATAAGCTTCTGACTTCTCCCACCATCCTTTCTTCTTCTCCTAGCATCTTCTATAGTAGAAGCAGGAGCTGGAACAGGATGAACAGTCTACCCTCCCCTAGCTGGCAACTTAGCTCA
TGCAGGCGCATCAGTAGACCTAACTATTTTCTCCCTTCATCTAGCTGGTGTATCCTCTATTCTAGGGGCTATTAATTTTATTACCACTATCATTAATATAAAACCACCCGCCATAACCCAATA
CCAAACACCCTTATTTGTGTGATCCGTACTTATCACAGCTGTTCTTCTTCTCCTTTCACTCCCAGTATTAGCTGCAGGTATTACAATACTACTAACTGATCGAAACCTAAATACAACTTTCTT
TGACCCCGCAGGAGGTGGAGACCCTATTCTCTACCAACATCTATTT

>RTSEA028-13|IC130112.3|Rattus tanezumi|COI-5P (RT Tarutao1)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA029-13|IC130110.1|Rattus tanezumi|COI-5P (RT Tarutao2)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGGACTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA030-13|IC130114.2|Rattus tanezumi|COI-5P (RT Tarutao3)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTTATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCCTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
CGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTCCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATCCTCTATCAACATCTATTT

>RTSEA031-13|IC130114.10|Rattus tanezumi|COI-5P (RT Tarutao4)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTAAGTATTTTAATTCGGGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA032-13|IC130114.11|Rattus tanezumi|COI-5P (RT Tarutao5)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGGGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA033-13|IC130107.8|Rattus tanezumi|COI-5P (RT Tarutao6)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA023-13|IC130107.4|Rattus tanezumi|COI-5P (RT Tarutao7)

ATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCATTGTTAC
AGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATAAACAAC
ATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCATGCTGG
AGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATATCAAAC
ACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTTCGATCC
TGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA002-13|UP100808.2|Rattus tanezumi|COI-5P (RT Trang)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATTGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTTTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA003-13|UP100723.3|Rattus tanezumi|COI-5P (RT Songkhla)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA004-13|IC120317.16|Rattus tanezumi|COI-5P (RT Yang1)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA005-13|IC120317.14|Rattus tanezumi|COI-5P (RT Yang2)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA

AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA006-13|IC120317.19|Rattus tanezumi|COI-5P (RT Yang3)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA007-13|IC120318.2|Rattus tanezumi|COI-5P (RT Adang1)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTACAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTCATACCGATAATAATCGGAGGCTTTGGAAACTGACTTGTGCCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
TGCCGGAGCATCTGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATAACCCAATA
TCAAACACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTTCTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA008-13|IC120320.12|Rattus tanezumi|COI-5P (RT Adang2)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTACAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTCATACCGATAATAATCGGAGGCTTTGGAAACTGACTTGTGCCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
TGCCGGAGCATCTGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATAACCCAATA

TCAAACACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTTCTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA009-13|IC120317.18|Rattus tanezumi|COI-5P (RT Adang3)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTACAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTCATACCGATAATAATCGGAGGCTTTGGAAACTGACTTGTGCCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
TGCCGGAGCATCTGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATAACCCAATA
TCAAACACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTTCTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA010-13|IC120320.11|Rattus tanezumi|COI-5P (RT Adang4)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTACAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTCATACCGATAATAATCGGAGGCTTTGGAAACTGACTTGTGCCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
TGCCGGAGCATCTGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATAACCCAATA
TCAAACACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTTCTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA011-13|IC120317.1|Rattus tanezumi|COI-5P (RT Adang5)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTACAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTCATACCGATAATAATCGGAGGCTTTGGAAACTGACTTGTGCCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAATCTAGCCCA
TGCCGGAGCATCTGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATAACCCAATA
TCAAACACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTTCTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA012-13|IC120318.121|Rattus tanezumi|COI-5P (RT Rawi1)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA013-13|IC120317.20|Rattus tanezumi|COI-5P (RT Rawi2)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA014-13|IC120318.10|Rattus tanezumi|COI-5P (RT Rawi3)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA015-13|IC120318.12|Rattus tanezumi|COI-5P (RT Rawi4)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA016-13|IC120216.3|Rattus tanezumi|COI-5P (RT Rawi5)

ACCCTTTATTTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA017-13|IC120213.14|Rattus tanezumi|COI-5P (RT Butong1)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTT
GATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA018-13|IC120215.6|Rattus tanezumi|COI-5P (RT Butong2)

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CCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCATT

GTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATAAA
CAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCATG
CCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATATC
AAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTTTG
ATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA019-13|IC130107.12|Rattus tanezumi|COI-5P (RT Tarutao8)

TATTTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAATGTCATTGTTA
CAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATACCGATAATAATCGGAGGCTTCGGAAACTGACTTGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATAAACAAT
ATAAGCTTTTGGCTGCTTCCCCCATCATTCTTACTTCTCCTAGCATCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCATGCCGG
AGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGAGCTATTAACTTTATCACTACTATTATTAATATAAAACCCCCTGCTATGACCCAATATCAAAC
ACCCCTATTTGTGTGATCTGTATTAATTACAGCTGTACTCCTACTTCTTTCACTACCAGTACTAGCAGCAGGTATCACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTTCGATCC
TGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA020-13|IC130106.5|Rattus tanezumi|COI-5P (RT Tarutao9)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA021-13|IC130107.7|Rattus tanezumi|COI-5P (RT Tarutao10)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA

AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA022-13|IC130107.5|Rattus tanezumi|COI-5P (RT Tarutao11)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA001-13|UP110819.5|Rattus tanezumi|COI-5P (RT Chumphon)

ACCCTCTATTTATTATTTGGTGCCTGAGCAGGAATAGTAGGAACAGCCTTGAGCATTCTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATTTATAATGTCA
TTGTTACAGCCCATGCATTCGTAATAATTTTCTTTATAGTTATGCCTATGATAATTGGAGGCTTCGGAAACTGGCTTGTACCACTAATGATTGGAGCCCCTGATATAGCATTCCCACGAATA
AACAATATAAGCTTTTGATTGCTTCCCCCATCATTTTTACTCCTTTTAGCATCATCTATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATACCCACCCTTAGCCGGTAACCTAGCCCA
TGCCGGAGCATCCGTTGACCTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCTTCTATCTTAGGAGCTATTAATTTTATCACCACTATCATCAATATAAAACCCCCTGCTATAACCCAATA
TCAAACCCCTCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTTTCACTACCAGTTTTAGCAGCAGGCATTACCATACTCCTCACAGATCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGACCCAATTCTCTATCAACACCTATTT

>RTSEA024-13|IC130113.4|Rattus tanezumi|COI-5P (RT Tarutao12)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA

TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA025-13|IC130107.9|Rattus tanezumi|COI-5P (RT Tarutao13)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA026-13|IC130105.12|Rattus tanezumi|COI-5P (RT Tarutao14)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGAGCTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>RTSEA027-13|IC130110.5|Rattus tanezumi|COI-5P (RT Tarutao15)

ACCCTCTATCTATTATTTGGTGCCTGAGCAGGAATAGTGGGAACAGCCTTAAGTATTTTAATTCGGACTGAACTAGGACAACCAGGAGCACTCCTAGGCGATGACCAAATCTATAACGTCA
TTGTTACAGCCCATGCATTCGTAATAATCTTCTTTATAGTCATACCAATAATAATCGGAGGCTTCGGAAACTGACTCGTACCACTAATGATCGGAGCCCCTGATATAGCATTCCCACGAATA
AACAACATAAGCTTTTGATTGCTTCCCCCATCATTCTTACTTCTCTTAGCGTCATCCATAGTAGAAGCCGGAGCCGGAACAGGATGAACAGTATATCCACCCTTAGCCGGTAATCTAGCCCA
TGCTGGAGCATCCGTTGACTTAACCATTTTCTCCCTTCACCTAGCTGGTGTATCCTCTATCTTAGGGGCTATTAACTTTATCACCACTATTATCAATATAAAACCCCCTGCCATAACCCAATA
TCAAACACCCCTATTTGTGTGATCCGTATTAATTACAGCTGTACTTCTACTTCTCTCACTACCAGTATTAGCAGCAGGTATTACCATACTCCTCACAGACCGAAACCTAAATACTACTTTTTT
CGATCCTGCTGGAGGCGGAGATCCAATTCTCTATCAACATCTATTT

>gi|299779467|gb|HM217482.1| Micromys minutus voucher BZ02 cytochrome oxidase subunit I (COXI) gene partial cds mitochondrial (out group)

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TTTACATGCTATTTGGTGCCTGAGCTGGAATAGTAGGAACAGCACTAAGCATTCTAATTCGAGCTGAATTAGGGCAACCCGGTGCTCTTCTAGGTGATGACCAAATCTATAATGTTATCGTT
ACTGCCCACGCATTCGTTATAATTTTCTTCATAGTGATGCCAATAATAATTGGCGGATTTGGAAACTGACTTGTCCCACTAATAATTGGAGCCCCTGACATAGCATTCCCCCGAATAAATAA
TATAAGTTTTTGACTTCTTCCTCCATCTTTCCTTCTCCTACTAGCCTCCTCAATAGTAGAAGCAGGAGCAGGAACAGGATGAACAGTTTACCCTCCCTTAGCCGGAAATTTAGCCCACGCAG
GTGCATCAGTTGATCTTACAATTTTCTCCCTTCACTTAGCTGGTGTTTCTTCAATTCTAGGGGCTATCAATTTTATTACTACTATCATTAACATAAAACCCCCTGCTATAACCCAATACCAAA
CCCCATTGTTTGTATGATCAGTATTAATTACAGCTGTCCTTCTTCTTCTTTCTCTCCCTGTACTCGCTGCCGGAATTACTATACTACTAACTGACCGAAATCTAAACACCACTTTCTTTGATCC
TGCAGGAGGAGGAGACCCAATCCTTTATCAACACCTATT-
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>gi|299779469|gb|HM217483.1| Micromys minutus voucher BZ07 cytochrome oxidase subunit I (COXI) gene partial cds mitochondrial (out group)

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CCCTTTACATGCTATTTGGTGCCTGAGCTGGAATAGTAGGAACAGCACTAAGCATTCTAATTCGAGCTGAATTAGGGCAACCCGGTGCTCTTCTAGGTGATGACCAAATCTATAATGTTATC
GTTACTGCCCACGCATTCGTTATAATTTTCTTCATAGTGATGCCAATAATAATTGGCGGATTTGGAAACTGACTTGTCCCACTAATAATTGGAGCCCCTGACATAGCATTCCCCCGAATAAA
TAATATAAGTTTTTGACTTCTTCCTCCATCTTTCCTTCTCCTACTAGCCTCCTCAATAGTAGAAGCAGGAGCAGGAACAGGATGAACAGTTTACCCTCCCTTAGCCGGAAATTTAGCCCACG
CAGGTGCATCAGTTGATCTTACAATTTTCTCCCTTCACTTAGCTGGTGTTTCTTCAATTCTAGGGGCTATCAATTTTATTACTACTATCATTAACATAAAACCCCCTGCTATAACCCAATACC
AAACCCCATTGTTTGTATGATCAGTATTAATTACAGCTGTCCTTCTTCTTCTTTCTCTCCCTGTACTCGCTGCCGGAATTACTATACTACTAACTGACCGAAATCTAAACACCACTTTCTTTGA
TCCTGCAGGAGGAGGAGACCCAATCCTTTATCAACACCTATT-
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APPENDIX 9. Inter-retinoid binding protein (IRBP) nuclear gene nucleotide sequences for both *R. tanezumi* (RT) and *M. surifer* (MS) analyzed in chapter 4. Showing both the names from BOLD and the abbreviation used in this study are given in brackets.

>RTSEA020-13|IC130106.5|Rattus tanezumi|IRBP (RT Tarutao9)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCC
TCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACGAGTGG
ATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCA
TGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTAC?ATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAA?GTCCT
GGGGGAGAGATACAGCGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGCTGAGGACATCGCTTACATCCTCAAGCAGATGCGCAGGGCCAT?GTGGTGGGTGA
GCGGACGGAGGGTGGCGCCCTAGACCTCCAGAAGCTGAGAATAGGTCAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGGA
AGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCCCTGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCTA
CAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCACCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCAG
GCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCTAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAGA
AGCTGCCCGGAGGGCCCTAGTGGACTCCGTGTTTCAGGTGTCCGTGCTGCCGGGCAATGTGGGCTACCTGCGCTTTGACAGATTTGCAGATGCCTCCGTG

>RTSEA023-13|IC130107.4|Rattus tanezumi|IRBP (RT Tarutao7)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCC
TCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACGAGTGG
ATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCA
TGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCC
TGGGGGAGAGATACAGTGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGC?GAGGACATCGCTTACATC?TCAAGCAGATGCGCAGGGCCATCGTGGTGGGTG
AGCGGACGGAGGGTGGCGCCCTGGACCTCCAGAAGCTGAGAATAGGCCAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGG
AAGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCCCTGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCT
ACAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCATCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCA
GGCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCCAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAG
AAGCTGCCCGGAGGGCCCTAGTGGACTCCGTGTTTCAGGTGTCCGTGCTGCCGGGCAATGTGGGCTACCTGCGCTTTGACAAATTTGCAGATGCCTCTGTG

>RTSEA033-13|IC130107.8|Rattus tanezumi|IRBP (RT Tarutao6)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCCTCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACAAGTGGATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCATGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCCTGGGGGAGAGATACAGTGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGCCGAGGACATCGCTTACATCCTCAAGCAGATGCGCAGGGCCATCGTGGTGGGTGAGCGGACGGAGGGTGGCGCCCTGGACCTCCAGAAGCTGAGAATAGGCCAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGGAAGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCCCTGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCTACAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCATCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCAGGCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCCAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAGAAGCTGCCCGGAGGGCCCTAGTGGACTCCGTGTTTCAGGTGTCCGTGCTGCCGGGCAATGTGGGCTACCTGCGCTTTGACAAATTTGCAGATGCCTCTGTG

>RTSEA031-13|IC130114.10|Rattus tanezumi|IRBP (RT Tarutao4)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCCTCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACGAGTGGATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCATGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCCTGGGGGAGAGATACAGCGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGCTGAGGACATCGCTTACATCCTCAAGCAGATGCGCAGGGCCATTGTGGTGGGTGAGCGGACGGAGGGTGGCGCCCTAGACCTCCAGAAGCTGAGAATAGGTCAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGGAAGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCC?TGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCTACAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCACCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCAGGCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCTAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAGAAGCTGCCCGGAGGGCCCTAGTGGACTCCGTGTTTCAGGTGTCCGTGCTGCCGGGCAATGTGGGCTACCTGCGCTTTGACAGATTTGCAGATGCCTCCGTG

>RTSEA030-13|IC130114.2|Rattus tanezumi|IRBP (RT Tarutao3)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCC
TCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACAAGTGG
ATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCA
TGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCC
TGGGGGAGAGATACAGTGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGC?GAGGACATCGCTTACATCCTCAAGCAGATGCGCAGGGCCAT?GTGGTGGGTG
AGCGGACGGAGGGTGGCGCCCTGGACCTCCAGAAGCTGAGAATAGG?CAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGG
AAGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCCCTGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCT
ACAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCATCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCA
GGCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCCAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAG
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>RTSEA029-13|IC130110.1|Rattus tanezumi|IRBP (RT Tarutao2)

TATGAAGAGTCACGAGATTCTGGGCATCTCGGACCCTCAGACGCTGGCCCATGTGCTGACAGTTGGAGTCCAGAGCTCTTTGAATGACCCACGTCTCTTCATCTCCTATGAGCCCAGTACCC
TCGAGGCCCCCCAGCAAGCACCAGCACTCACCGACCTCACCCGAGAAGAGCTACTGGCCCAGATACAGAGGAACATCCGCCATGAGGTTCTTGAGGATAACGTGGGCTACCTACAAGTGG
ATGATCTCCCTGGACAGGAGGTACTGAGTGAGCTGGGGGAGTTCCTAGTGAGCCATGTGTGGGAGCAGCTCATGGGCACCTCCTCCTTGGTGCTGGATCTCCGTCACTGTGCTGGTGGCCA
TGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACAGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCC
TGGGGGAGAGATACAGTGCTGACAAGGATGTGGTGGTCCTCACCAGTGGACACACTGGGGGAGTAGC?GAGGACATCGCTTACATCCTCAAGCAGATGCGCAGGGCCATCGTGGTGGGTG
AGCGGAGGGAGGGTGGCGCCCTGGACCTCCAGAAGCTGAGAATAGGCCAGTCCGACTTCTTCCTTACAGTGCCTGTGTCCAGGTCCCTGGGGCCCCTAGGTGGAGGAGGCCAAACGTGGG
AAGGCAGCGGGGTGCTGCCCTGTGTGGGGATACCTGCAGAGCAAGCCCTAGAAAAGGCCCTGGCCATCCTCACCCTGCGTCGTGCCCTGCCAGGCGTTGTCCTCCGACTCCAGGAAGCCCT
ACAGGACTATTACACATTAGTGGACCGAGTGCCGGGCCTGCTGCACCATCTGGCCAGCATGGACTACTCGGCCGTGGTCTCCGAAGAGGACCTGGTGACAAAGCTCAATGCTGGTTTGCA
GGCTGTGTCGGAGGATCCCAGGCTCCTGGTGAGAGCCACCGGACCCAGAGAAACCCCCTCAAGACCTGAGACTGGCCCTAACGAGCCACCAGCAGTCACCCCTGAGGTGCCCAAGGAAG
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>RTSEA027-13|IC130110.5|Rattus tanezumi|IRBP (RT Tarutao15)

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>RTSEA026-13|IC130105.12|Rattus tanezumi|IRBP (RT Tarutao14)

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>RTSEA024-13|IC130113.4|Rattus tanezumi|IRBP (RT Tarutao12)

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>RTSEA014-13|IC120318.10|Rattus tanezumi|IRBP (RT Rawi3)

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>RTSEA013-13|IC120317.20|Rattus tanezumi|IRBP (RT Rawi2)

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>RTSEA012-13|IC120318.121|Rattus tanezumi|IRBP (RT Rawi1)

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>RTSEA008-13|IC120320.12|Rattus tanezumi|IRBP (RT Adang2)

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>RTSEA007-13|IC120318.2|Rattus tanezumi|IRBP (RT Adang1)

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>RTSEA054-13|IC130113.3|Maxomys surifer|IRBP (MS Tarutao8)

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>RTSEA053-13|IC130114.8|Maxomys surifer|IRBP (MS Tarutao7)

TATGAAGAGTCATGAGATTCTGGGCATCTCAGACCCTCAGACGCTGGCCCACGTGCTGACAGCCGGAGT?CAGAGCTCTTTGAATGACCCGCGTCTCTTCATCTCCTACGAGCCCAGTACCC
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TGTCTCTGGGATCCCTTATGTCATCTCCTACTTGCACCCTGGGAACACCGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCC
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TATGAAGAGTCATGAGATTCTGGGCATCTCAGACCCTCAGACGCTGGCCCACGTGCTGACAGCCGGAGTCCAGAGCTCTTTGAATGACCCGCGTCTCTTCATCTCCTATGAGCCCAGTACC
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AGGCTGTGTCAGAGGATCCTAGGCTCCTGGTGAGAGCCACTGGACCCAGAGAAACCTCCTCAAGACCTGAGATGGGACCTAATGACCCCCCAGCAGTCACCCCTGAGGTGCCCAAGGACG
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GGCTGTGTCAGAGGATCCTAGGCTCCTGGTGAGAGCCACTGGACCCAGAGAAACCTCCTCAAGACCTGAGATGGGACCTAATGACCCCCCAGCAGTCACCCCTGAGGTGCCCAAGGAAGA
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TATGAAGAGTCATGAGATTCTGGGCATCTCAGACCCTCAGACGCTGGCCCACGTGCTGACAGCCGGAGTACAGAGCTCTTTGAATGACCCGCGTCTCTTCATCTCCTACGAGCCCAGTACC
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TATGAAGAGTCATGAGATTCTGGGCATCTCAGACCCTCAGACGCTGGCCCACGTGCTGACAGCCGGAGT?CAGAGCTCTTTGAATGACCCGCGTCTCTTCATCTCCTACGAGCCCAGTACCC
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TGTCTCTGGGATC?CTTATGTCATCTCCTACTTGCACCCTGGGAACACCGTCTTGCACGTGGATACCATCTACGATCGGCCCTCCAACACCACCACAGAGATCTGGACCTTGCCTAAGGTCC
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>gi|299779701|gb|HM217599.1| Micromys minutus voucher BZ07 interphotoreceptor retinoid binding protein (IRBP) gene partial cds (Out group)

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Student ID: 5410220127

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